

OM protein - protein search, using sw model			
Run on:	May 5, 2003, 16:56:07 ; Search time 44 Seconds		
Post-processing:	(without alignments)		
Database :	US-09-142-524D-3		
Scoring table:	BLOSUM62		
Searched:	Gapop 10.0 , Gapext 0.5		
Total number of hits satisfying chosen parameters:	283224		
Minimum DB seq length:	0		
Maximum DB seq length:	200000000		
Post-processing:	Minimum Match 0%		
	Maximum Match 100%		
	Listing first 45 summaries		
PIR 73:*			
1: pir1:*			
2: pir2:*			
3: pir3:*			
4: pir4:*			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
Result No.	Score	Query Match Length	DB ID
1	188	26.4	374 2 JC2124
2	188	26.4	374 2 JC2123
3	148.5	20.9	514 2 JC2498
4	148.5	20.9	514 2 JC2120
5	118.5	16.7	514 2 JC7100
6	110.5	15.5	542 2 T06728
7	107.5	15.1	507 2 JC7366
8	104.5	14.7	463 2 T46165
9	103	14.5	404 2 S12209
10	99	13.9	472 2 T5156
11	98.5	13.9	396 2 A39099
12	97	13.6	397 2 C39099
13	97	13.6	T00856
14	97	13.6	459 2 G86278
15	95.5	13.4	404 2 T05556
16	94.5	13.3	431 2 R86179
17	94.5	13.3	526211
18	93	13.1	398 2 B39099
19	93	13.1	450 2 T09524
20	93	13.1	397 2 B53240
21	92	12.9	398 2 B53240
22	92	12.9	368 2 G86427
23	91.5	12.9	398 2 T07058
24	91	12.8	392 2 D53240
25	89	12.5	438 2 S29612
26	89	12.5	243335
27	88	12.4	T05240
28	84	11.8	R85148
29	11.8		
ALIGNMENTS			
RESULT 1			
JC124			
major allergen Cry j I precursor (clone pCC-15) - Japanese cedar			
C;Species: Cryptomeria japonica (Japanese cedar)			
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 21-Jul-2000			
C;Accession: JC124			
R;Sone, T.; Komiyama, N.; Shimizu, K.; Kusakabe, T.; Morikubo, K.; Kino, K.			
Biochem. Biophys. Res. Commun. 199, 619-625, 1994			
A;Title: Cloning and sequencing of cDNA coding for Cry j I, a major allergen of Japanese cedar			
A;Reference number: JC2123; MUID:94183234; PMID:8135802			
A;Accession: JC2124			
A;Molecule type: mRNA			
A;Residues: 1-374 <SON>			
A;Cross-references: GB:D26545; NID:9493633; PID:9493634			
A;Experimental source: pollen			
A;Note: the authors described carbohydrate binding site for residue 279			
C;Superfamily: glycoprotein; pollen			
F;1-21/Domain: signal sequence #status predicted <SIG>			
F;22-374/Product: major allergen Cry j I (clone pCC-15) #status predicted <MAT>			
F;156,191,293,354/Binding site: carbohydrate (Asn) (covalent) #status predicted			
Query Match Score 188; DB 2; Length 374;			
Best Local Similarity 71.2%; Pred. No. 1.9e-12; Indels 0; Gaps 0;			
Matches 37; Conservative 4; Mismatches 11;			
Query 73 RPLWITFSNNMKLKKMNYIAGYKTFGRRAEVSVVHNGKFIRRDVGIL 124			
Db 87 RPLWITFSNNMKLKKMNYIAGYKTFGRRAEVSVVHNGKFIRRDVGIL 138			
RESULT 2			
JC2123			
major allergen Cry j I precursor (clone pCC-2-2) - Japanese cedar			
C;Species: Cryptomeria Japonica (Japanese cedar)			
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 21-Jul-2000			
C;Accession: JC2123; PC2065			
R;Sone, T.; Komiyama, N.; Shimizu, K.; Kusakabe, T.; Morikubo, K.; Kino, K.			
Biochem. Biophys. Res. Commun. 199, 619-625, 1994			
A;Title: Cloning and sequencing of cDNA coding for Cry j I, a major allergen of Japanese cedar			
A;Reference number: JC2123; MUID:94183234; PMID:8135802			
A;Accession: JC2123			
A;Molecule type: mRNA			
A;Residues: 1-374 <SON>			
A;Cross-references: GB:D26544; NID:9493631; PID:9493632			
A;Experimental source: pollen			
A;Accession: PC2065			
A;Molecule type: protein			
A;Residues: 22-53; 219-232; 236-258; 299-307; 346-372 <SO2>			
A;Note: the authors described carbohydrate binding site for residue 279			
C;Superfamily: pectate lyase; pollen			
C;Keywords: glycoprotein; pollen			

F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-374/Product: major allergen Cry J I (clone pCCr-2-2) #status predicted <MAT>
 F;158,191,293,354/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.4%; Score 188; DB 2; Length 374;
 Best Local Similarity 71.2%; Pred. No. 1_9e-12; Mismatches 11; Indels 4; Gaps 0;
 Matches 37; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
 QY 73 RPWLIIFSGNMNTKLKMPMYTAGYKTFDGRRAEVSVYHVNAGAKFIRRVDGI 124
 Db 87 RPWLIIFSGNMNTKLKMPMYTAGYKTFDGRRAEVSVYHVNAGAKFIRRVDGI 124

Db 87 RPWLIIFSGNMNTKLKMPMYTAGYKTFDGRRAEVSVYHVNAGAKFIRRVDGI 124

RESULT 3

S16730 CRY J II protein - Japanese cedar

C;Species: Cryptomeria japonica (Japanese cedar)

C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999

C;Accession: S48730 R.Namba, M.; Kurose, M.; Torigoe, K.; Hino, K.; Taniguchi, Y.; Fukuda, S.; Usui, M.; Kurihara, T.; Yokoyama, M.; Komiyama, N.; Okano, M.; Kino, K.

FEBs Lett. 355, 124-128, 1994

A;Title: Molecular cloning of the second major allergen, cry j II, from Japanese cedar P

A;Reference number: S48730; MUID:95010777; PMID:726035

A;Accession: S48730 A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1_514 <NAM>

A;Cross-references: GB:D37765; NID:9577695; PIDN:BAA07021.1; PID:d1007598; PID:9577696

Query Match 20.9%; Score 148.5; DB 2; Length 514;
 Best Local Similarity 41.4%; Pred. No. 4_9e-08; Mismatches 8; Indels 21; Gaps 2;
 Matches 41; Conservative 8; Mismatches 21; Indels 29; Gaps 2;

Qy 31 IDIFASKNPHIQKNTIGTGRWKNNRRIWLOFAKLTGFTLGRPLWIFSGNMNTKLKMP 90

Db 236 IDIFASKNPHIQKNTIGTGRWKNNRRIWLOFAKLTGFTLGRPLWIFSGNMNTKLKMP 90

Qy 91 MYIAGYKTFDGGRAEVSVYHVNAGAKFIRRVDGI 123

Db 273 ICGPGHGIGISLGLRENSRAEVSVYHVNAGAKFIRRVDGI 311

RESULT 4

JC2498 second major allergen CRY J II precursor - Japanese cedar

C;Species: Cryptomeria japonica (Japanese cedar)

C;Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 21-Jul-2000

C;Accession: JC2498; PC2246; A60147 R.Komiya, N.; Sone, T.; Shimizu, K.; Moritubo, K.; Kino, K.

Biochem. Biophys. Res. Commun. 201, 1031-1038, 1994

A;Title: cDNA Cloning and expression of Cry J II, the second major allergen of Japanese cedar

A;Reference number: JC2498; MUID:94271186; PMID:8002972

A;Accession: JC2498 A;Molecule type: mRNA

A;Residues: 1_514 <NOM>

A;Cross-references: DDBJ:D29772; NID:9506857; PIDN:BAA06172.1; PID:9506858

A;Accession: PC2346 A;Molecule type: protein

A;Residues: 52-61 <K02>

R.Sakaguchi, M.; Inouye, S.; Taniai, M.; Ando, S.; Usui, M.; Matuhasi, T.

Allergy 45, 319-322, 1990

A;Title: Identification of the second major allergen of Japanese cedar pollen.

A;Accession: A60147; MUID:90342988; PMID:2382797

A;Molecule type: protein

A;Residues: 55-64 <SAK>

C;Keywords: glycoprotein; pollen

F;1-54/domain: signal sequence #status predicted <SIG>

F;55-54/domain: Product: second major allergen Cry J #status predicted <MAT>

F;429, 460, 472/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.9%; Score 148.5; DB 2; Length 514;

Best Local Similarity 41.4%; Pred. No. 4_9e-08;

Score 148.5; DB 2; length 514;

Best local similarity 41.4%; pred. no. 4_9e-08;

Best local similarity 41.4%; pred. no. 4_9e-08;

Best local similarity 41.4%; pred. no. 4_9e-08;

Matches 41; Conservative 8; Mismatches 21; Indels 29; Gaps 2;

Qy 31 IDIFASKNPHIQKNTIGTGRWKNNRRIWLOFAKLTGFTLGRPLWIFSGNMNTKLKMP 90

Db 236 IDIFASKNPHIQKNTIGTGRWKNNRRIWLOFAKLTGFTLGRPLWIFSGNMNTKLKMP 90

Qy 91 MYIAGYKTFDGGRAEVSVYHVNAGAKFIRRVDGI 123

Db 273 ICGPGHGIGISLGLRENSRAEVSVYHVNAGAKFIRRVDGI 311

RESULT 5

JC7100 polygalacturonase Cha o 2 - Japanese cypress

C;Species: Chamaecyparis obtusa (Japanese cypress)

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000

C;Accession: JC7100; PC7026 R.Mori, T.; Yokoyama, M.; Komiyama, N.; Okano, M.; Kino, K.

Biochem. Biophys. Res. Commun. 263, 166-171, 1999

A;Title: Purification, identification, and cDNA cloning of Cha o 2, the second major all

A;Accession: JC7100 A;Molecule type: mRNA

A;Residues: 1_514 <MOR>

A;Accession: PC7026 A;Molecule type: protein

A;Residues: 51-62 <MO2>

Query Match 16.7%; Score 118.5; DB 2; Length 514;

Best Local Similarity 35.4%; Pred. No. 8_3e-05; Mismatches 25; Indels 29; Gaps 2;

Matches 35; Conservative 10; Mismatches 25; Indels 29; Gaps 2;

Qy 31 IDIFASKNPHIQKNTIGTGRWKNNRRIWLOFAKLTGFTLGRPLWIFSGNMNTKLKMP 90

Db 236 IDIFASKNPHIQKNTIGTGRWKNNRRIWLOFAKLTGFTLGRPLWIFSGNMNTKLKMP 90

Qy 91 MYIAGYKTFDGGRAEVSVYHVNAGAKFIRRVDGI 123

Db 273 ICGPGHGIGISLGLRENSRAEVSVYHVNAGAKFIRRVDGI 311

RESULT 6

T06728 peptate lyase (EC 4.2.2.2) F28P10_100 - Arabidopsis thaliana

N;Alternate names: Protein F28P10_100

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999

C;Accession: T06728 R.Queutier, F.; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigau, E.; Sone, T.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigau, E.; Reference number: T06728

A;Title: Submission to the Protein Sequence Database, April 1999

A;Accession: T06728 A;Molecule type: DNA

A;Residues: 1_514 <UEK>

A;Cross-references: EMBL:AL099655

A;Experimental source: cultivar Columbia; BAC clone F28P10

C;Genetics:

A;Map position: 3

A;Introns: 467/2; 346/3; 413/2; 480/2

A;Note: F28P10_100

C;Superfamily: peptate lyase LAT59

C;Keywords: carbon-oxygen lyase

Query Match 15.5%; Score 110.5; DB 2; Length 542;

Best Local Similarity 43.3%; Pred. No. 0_00064; Mismatches 20; Indels 5; Gaps 2;

Matches 26; Conservative 9; Mismatches 20; Indels 5; Gaps 2;

Qy 67 FTLMGRRPWITIFSGNMNTKLKMPMYTAGYKTFDGRRAEVSVYHVNAGAKFIRRVDGI 124

Db 139 YGVIOBEPFLWIVFSSNMILRKELINSYKTDGRG--SAVHITNGCILQYVQHII 195

RESULT 7

JC7366
 Jun a 2 protein - mountain cedar
 C;Species: Juniperus ashei (mountain cedar)
 C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000
 C;Accession: JC7366; PC7093
 R;Yokoyama, M.; Miyahara, M.; Shimizu, K.; Kino, K.; Tsunoo, H.
 Biochem. Biophys. Res. Commun. 275, 195-202, 2000
 A;Title: Purification, identification, and cDNA cloning of Jun a 2, the second major all
 A;Reference number: JC7366
 A;Accession: JC7366
 A;Molecule type: mRNA
 A;Residues: 1-507 <YOK>
 A;Cross-references: GB:AU404653
 A;Accession: PC7093
 A;Molecule type: protein
 A;Residues: 55-63 <Y0>
 C;Comment: This protein, a second major allergen of mountain cedar pollen, which is invc
 o the polygalacturonase family.
 C;Keywords: glycoprotein; pollen

Query Match 15.1%; Score 107.5; DB 2; Length 507;
 Best Local Similarity 32.3%; Pred. No. 0.0012;
 Matches 32; Conservative 13; Mismatches 25; Indels 29; Gaps 2;

Qy 31 IDRFSKKNFLQKNTIGTGRWKRNNIWIQFAKLTGFTLGRRLWIFPSGNKNUKMP 90
 Db 237 IDRFSKRFIEKCTGTG-----DDCAVGTGSSNITIKDL 273

Db 274 TCGPRHGMSTGSLKGNSRSEVSFVHLGAKFTDONGL 312

RESULT 8
 T46155
 Pectate lyase-like protein - Arabidopsis thaliana
 N;Alternate names: protein T4D2.120
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
 C;Accession: T46155
 R;Nakamura, G.; Fartmann, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
 submitted to the Protein Sequence Database, December 1999
 A;Reference number: 223025
 A;Accession: T46155
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-463 <YNA>
 A;Cross-references: EMBL:AL132958
 A;Experimental source: cultivar Columbia; BAC clone T4D2
 C;Genetics:
 A;Map position: 3
 A;Introns: 2/2; 11/2; 182/1; 265/3; 329/3; 399/2
 A;Note: T4D2.120
 C;Superfamily: pectate lyase LAT59

Query Match 14.7%; Score 104.5; DB 2; Length 463;
 Best Local Similarity 30.5%; Pred. No. 0.0024;
 Matches 32; Conservative 8; Mismatches 32; Indels 33; Gaps 3;

Qy 52 WKNRNTWL-----QFAKLTG-----FILGRRPLWIF 79
 Db 66 WPNHNGQGLADCGIGGQYALGGKGSGQFYFVTDSSDDAVNPKPGLTRGVQEPPLWIVF 125

Qy 80 SGNNNTKLKMPMYIAGKTFDGRRAEVSYHVNNGAKFIRRDGTI 124
 Db 126 PSNNMMKLUKQBLIFNSYKTLDRGANHVTG-GGCILQYVSNII 169

RESULT 9
 S12209
 pectate lyase (EC 4.2.2.2) - tomato
 C;Species: Lycopersicon esculentum (tomato)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 23-Jul-1999

C;Accession: S12209
 R;Budelier, K.A.; Smith, A.G.; Gasser, C.S.
 Mol. Gen. Genet. 224, 183-192, 1990
 A;Title: Regulation of a stylar transmitting tissue-specific gene in wild-type and trans
 A;Reference number: S12209; MUID:91117185; PMID:2277637
 A;Accession: S12209
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-104 <YUD>
 A;Cross-references: GB:J55193; NID:gi19161; PIDN:CAA38979.1; PID:gi19162
 C;Superfamily: pectate lyase LAT59
 C;Keywords: carbon-oxygen lyase

Query Match 14.5%; Score 103; DB 2; Length 404;
 Best Local Similarity 30.8%; Pred. No. 0.0029;
 Matches 33; Conservative 13; Mismatches 31; Indels 30; Gaps 4;

Qy 28 GRRIDFASKNHFQKNTIGTGRWKNNIWIQFAKLTGFIM 70
 Db 67 GKSPSAFSYCAIGRKAIG---GKNGRILYVWIDSGNNDPWPWPKPGTIRHA-----VI 116

Qy 71 GRRPLWIFPSGNNTKLKMPMYIAGKTFDGRRAEVSYHVNNGAKFI 117
 Db 117 QDEPLWIFKRDWVQQLKBLVMSYKTDGRGAS--WHISGPCI 160

RESULT 10
 T51456
 Pectate lyase-like protein - Arabidopsis thaliana
 N;Alternate names: protein F2G14_230
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
 C;Accession: T51456
 R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
 Submitted to the Protein Sequence Database, August 2000
 A;Reference number: 225394
 A;Accession: T51456
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-472 <SAT>
 A;Cross-references: EMBL:AL391146
 A;Experimental source: cultivar Columbia; BAC clone F2G14
 C;Genetics:
 A;Map position: 5
 A;Introns: 65/2; 316/3; 398/3
 A;Note: F2G14_230
 C;Superfamily: pectate lyase LAT59

Query Match 13.9%; Score 99; DB 2; Length 472;
 Best Local Similarity 28.2%; Pred. No. 0.0094;
 Matches 29; Conservative 17; Mismatches 41; Indels 16; Gaps 3;

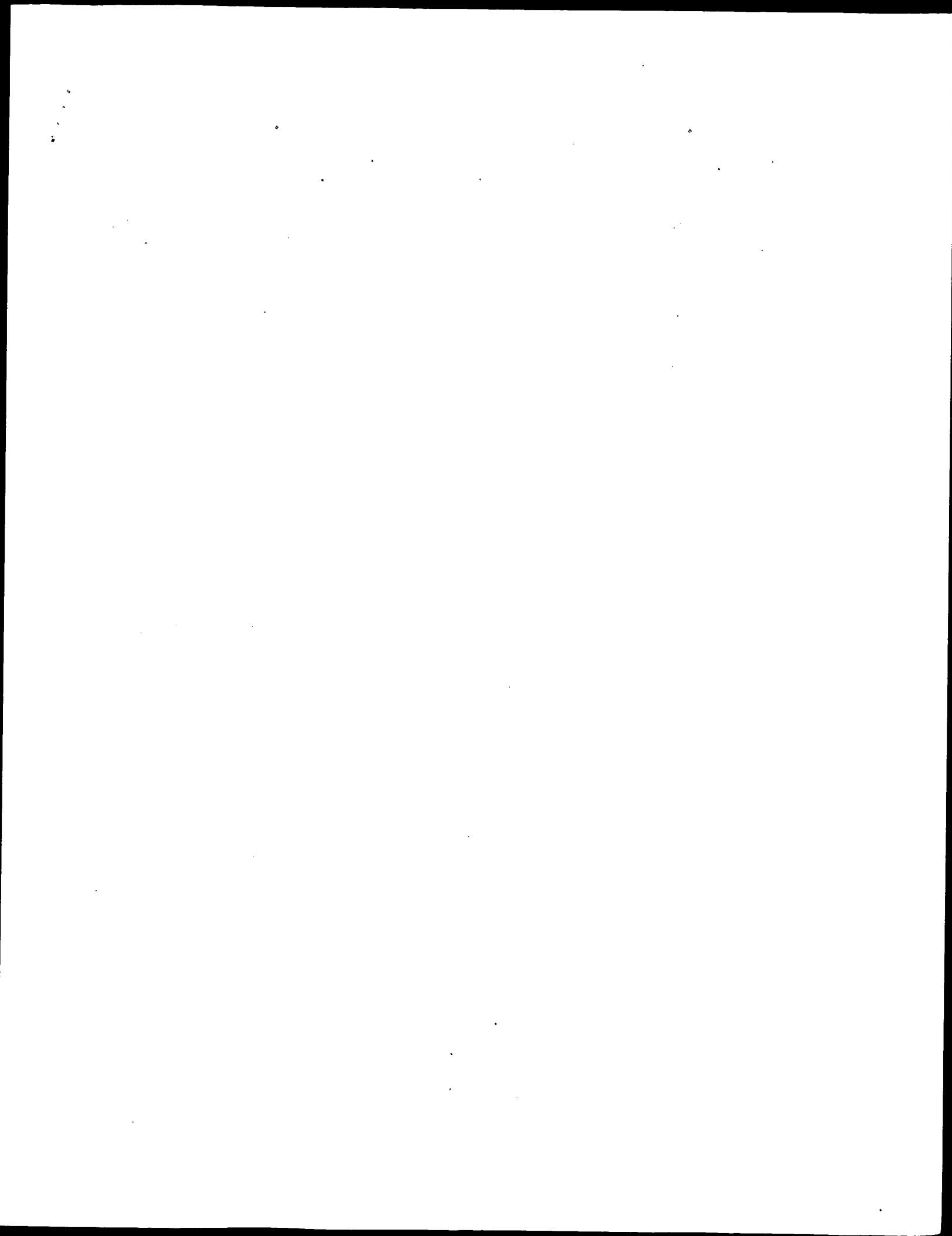
Qy 34 FASKNHFQKNTIGTGR--WKNRNIWIQFAKLTG-----TGFTLGRRLWIF 79
 Db 134 WAKRKXKTRGRGFGHRTGKAKRIVYVTSNLDEMWPKPGTIRHVAQEPFLWIF 193

Qy 80 SGNNNTKLKMPMYIAGKTFDGRRAEVSYHVNNGAKFIRRDGTI 120
 Db 194 KNDMSIRNLQNBLLINSHKTIDARGANHVHAGGITMOFKNV 236

RESULT 11
 A39099
 Allergen Amb a 1.1 precursor - common ragweed
 C;Species: Ambrosia artemisiifolia (common ragweed)
 C;Date: 27-Nov-1991 #sequence_revision 03-Apr-1992 #text_change 29-Sep-1999
 C;Accession: A39099; A60895; A53240
 R;Raffan, T.; Griffith, T.J.; Kuo, M.; Bond, J.F.; Rogers, B.L.; Klapper, D.G.
 J. Biol. Chem. 266, 1229-1236, 1991
 A;Title: Cloning of Amb a I (antigen E), the major allergen family of short ragweed poll
 A;Reference number: A39099; MUID:gi1093235; PMID:1702434
 A;Accession: A39099
 A;Molecule type: mRNA

A;Residues: 1-396 <RAF>
 A;Cross-references: GB:M63116
 A;Residues: 256-273,292-303 'W' 305-306 <SMI>
 R;Griffith, J.J.; Olson, J.R.; Klapper, D.G.
 M.J.; Immunol. 25, 355-365, 1988
 A;Title: Monoclonal antibodies to denatured ragweed pollen allergen Amb a I: characteriz
 a;I
 A;Reference number: A60895; MUID:88288254; PMID:2456454
 A;Accession: A60895
 A;Molecule type: protein
 A;Residues: 256-273,292-303 'W' 305-306 <SMI>
 R;Griffith, J.J.; Pollock, D.G.; Rogers, B.L.; Nault, A.K.
 Int. Arch. Allergy Appl. Immunol. 96, 296-304, 1991
 A;Title: Sequence polymorphism of Amb a I and Amb a II, the major allergens in Ambrosia
 A;Reference number: A53240; MUID:92234570; PMID:1809687
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Accessories: 1-396 <GR>
 A;Cross-references: GB:M80558; NID:9166434; PIDN:AAA32665.1; PID:9166435
 C;Superfamily: pectate lyase LAT59
 C;Keywords: glycoprotein; pollen
 F,36/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 13.9%; Score 98.5; DB 2; Length 396:
 Best Local Similarity 34.7%; Pred. No. 0.0087;
 Matches 26; Conservative 12; Mismatches 22; Indels 15; Gaps 3;
 Qy 73 RPWLIIFSGNNKIKLKPMPYTAGKTFDGRRAEVSYVH---VNGAK---FIRRVD---- 121
 Db 113 RPWLIIFRDWYVRLDKEMVNSDKTIDGRGAKVETINAGFTLNGKTVNTHNMHDVK 172
 Qy 122 ---GIAAYONPAS 132
 Db 173 VNFEGGLIKSNDGFAA 187
 RESULT 12
 C53240
 allergen Amb a I,3 precursor - common ragweed
 C;Species: Ambrosia artemisiifolia (common ragweed)
 C;Accession: C53240
 C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 18-Sep-1998
 R;Griffith, J.J.; Pollock, D.G.; Rogers, B.L.; Nault, A.K.
 Int. Arch. Allergy Appl. Immunol. 96, 296-304, 1991
 A;Title: Sequence polymorphism of Amb a I and Amb a II, the major allergens in Ambrosia
 A;Reference number: A53240; MUID:92234570; PMID:1809687
 A;Accession: C53240
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Accessories: 1-397 <GR>
 A;Cross-references: GB:M80560
 C;Superfamily: pectate lyase LAT59
 C;Keywords: pollen
 Query Match 13.6%; Score 97; DB 2; Length 397;
 Best Local Similarity 29.5%; Pred. No. 0.013;
 Matches 31; Conservative 7; Mismatches 33; Indels 34; Gaps 3;
 Qy 52 WKNRRIWQ----FAXLT----- 131
 Db 61 WENNRQALADCAQGFKATGYGGKGWDVYTISNLDDVANPREGTRFAAQNRLWII 120
 Qy 80 SGNNKIKLKPMPYTAGKTFDGRRAEVSYVHNGA---KFIRR 124
 Db 121 KNDMVNINQNOELVNSDKTIDGRGVKEI--INGSLTLMVNKNII 163
 RESULT 14
 T00856
 pectate lyase (EC 4.2.2.2) T20F6.14 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: T00856; A84440
 R;Griffith, J.J.; Klapper, D.G.; Rogers, B.L.; Nault, A.K.
 R;Rounseley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
 submitted to the EMBL Data Library, March 1998
 A;Description: Arabidopsis thaliana chromosome II BAC T20F6 genomic sequence.
 A;Reference number: Z14206
 A;Accession: T00856
 A;Status: translated from GR/EMBL/DDBJ
 A;Molecule type: DNA
 A;Cross-references: ROU>
 A;Experimental source: cultivar Columbia (mouse-ear cress)
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; vanaken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.;
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: A84420
 A;Status: preliminary
 A;Molecule type: DNA
 A;Accessories: 1-455 <STO>
 A;Cross-references: GB:AE002093; NID:92947069; PIDN: AAC05350.1; GSPDB:GN00139
 C;Genetics: A;Gene: At2g02720
 A;Map position: 2
 A;Introns: 6/2; 295/3; 376/3
 A;Note: T20F6.14
 C;Superfamily: pectate lyase LAT59
 C;Keywords: carbon-oxygen lyase
 Query Match 13.6%; Score 97; DB 2; Length 455;
 Best Local Similarity 46.2%; Pred. No. 0.015;
 Matches 24; Conservative 9; Mismatches 13; Indels 6; Gaps 3;
 Qy 73 RPWLIIFSGNNKIKLKPMPYTAGKTFDGRRAEVSYVHNGA---KFIRR 120
 Db 166 RPWLIIFARSHMIKLUQELITNDKTDGSGAKI-YI-TGGAGLTLQFVRN 215
 RESULT 15
 C39099
 allergen Amb a I,3 - common ragweed
 C;Species: Ambrosia artemisiifolia (common ragweed)
 C;Date: 27-Nov-1991 #sequence_revision 03-Apr-1992 #text_change 29-Sep-1999
 C;Accession: C39099

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 01-Mar-2002
 C;Accession: G66278
 R;Theologis, A.; Becker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huijar, L.
Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; A;Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; A;Title: Sequence and analysis of chromosome 1 of the Plant *Arabidopsis*.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: G66278
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-59 <STO>
 A;Cross-references: GB:AB005172; NID:97262684; PIDN:AAF43942.1; GSPDB:GN00141
 C;Genetics:
 A;Map position: 1
 C;Superfamily: pectate lyase LAT59
 Query Match 13.4%; Score 95.5; DB 2; Length 459;
 Best Local Similarity 28.6%; Pred. No. 0.022; 9; Mismatches 28; Indels 43; Gaps 4;
 Matches 32; Conservative 32; Goncharov 32;
 Qy 50 RRWKNRRIWLQFAKLTGFTL-MGRR----- 73
 Db 115 RWWAANR----KKLADCVLGFGRRRTGGKGDPVYVKAASNDL1NPKGTLRAVTRD 169
 Qy 74 -PLWILIFSGNNNIKLNKMPMTAGYKTFDGRRAEVSTVHNGAKFRRVDGII 124
 Db 170 GFLWILIFARSMWIKLQELIMITSDKITDGRCARY-YIMEGAGLTLQFVNNTVI 220
 Search completed: May 5, 2003, 16:59:58
 Job time : 55 sec8



OM protein - protein search, using SW model

Perfect score: US-09-142-524D-3

Sequence: 711 MKVTVAFFNQGPNNRVEFIKR.....KFIRRVUDGITAAYQNPASWK 134

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	188	26.4	374	1 SBP_CRYJA
2	150	21.1	1 MPAI_JUNJAS	
3	148.5	20.9	514	1 MPB2_CRYJA
4	143	20.1	346	1 MPAL_CUPAR
5	142	20.0	375	1 MPAL_CHAOB
6	103	14.5	404	1 9612_LYCLES
7	98.5	13.9	396	1 MP11_AMBAR
8	97	13.6	397	1 MP11_AMBAR
9	93	13.1	397	1 PERL_TOBAC
10	93	13.1	398	1 MP12_AMBAR
11	92	12.9	392	1 MP12_AMBAR
12	91	12.8	398	1 PRS6_LYCLES
13	89	12.5	1 MP14_AMBAR	
14	89	12.5	434	1 PERL_TOILO
15	82.5	11.6	449	1 PRS9_LYCLES
16	81.5	11.5	234	1 A29B_DROME
17	80.5	11.3	605	1 PRAC_MEPTEX
18	71	10.0	2710	1 TOXA_CLODI
19	70.5	9.9	622	1 CRAC_BACTU
20	69.5	9.8	338	1 YOK8_YEAST
21	68.5	9.6	234	1 A29B_DROSTI
22	68.5	9.6	551	1 CHIT_NPYAC
23	67.5	9.5	985	1 ASGU_ASFOR
24	67.5	9.5	1070	1 YIVV4_YEAST
25	67	9.4	757	1 FXI1_RHIME
26	66.5	9.4	110	1 Y12K_SHSV4
27	66	9.3	375	1 Y48D_RHLSN
28	66	9.3	382	1 PRY7_BACUL
29	66	9.3	646	1 NOQO_RHJS3
30	65	9.1	576	1 DPEP_SOILU
31	65	9.1	726	1 YB1718_schizosaccharomyces_pasteuri
32	65	9.1	781	1 TL22_CHICK
33	64.5	9.1	1 CLPP_CHLIEU	

RESULT 1
SBP_CRYJA
ID SBP_CRYJA STANDARD; PRT; 374 AA.
AC P18632;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Sugi basic protein precursor (SBP) (Major allergen Cry j 1) (Cry j 1).
OS Cryptomeria japonica (Japanese cedar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Cupressaceae; Cryptomeria.
OX NCBI_TaxID=3369;

RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Pollen; MEDLINE=94183234; PubMed=8135802;
RX Sone T., Koniymaya N., Shimizu K., Kusakabe T., Morikubo K.,
RA Kino T.; Cloning and sequencing of cDNA coding for Cry j 1, a major allergen
RT of Japanese cedar pollen.; Kurimoto M., Sakaguchi M., Inouye S.,
RL Biochem. Biophys. Res. Commun. 199:619-625(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pollen; Namba M., Kurose M.; Torigoe K., Fukuda S., Kurimoto M.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 22-41.
RC TISSUE=Pollen; MEDLINE=8901257; PubMed=3181436;
RX Tannai M., Ando S., Usui M., Kurimoto M., Inouye S.,
RA Matsumoto T.; N-terminal amino acid sequence of a major allergen of Japanese cedar
RT pollen (Cry j 1); PolLEN (Cry j 1); "PolLEN (Cry j 1)." ;
RL Lett. 239:329-332(1988).
RN [4]
RP CARBOHYDRATES.
RC TISSUE=Pollen; MEDLINE=9503748; PubMed=7920021;
RX Hijikata A., Matsumoto I., Kojima K., Ogawa H.;
RT "Antigenicity of the oligosaccharide moiety of the Japanese cedar
(Cryptomeria japonica) pollen allergen, Cry j 1";
RT (Cryptomeria japonica) pollen allergen, Cry j 1; Int. Arch. Allergy Immunol. 105:198-202(1994).
RL [5]
RN STRUCTURE OF CARBOHYDRATES.
RC TISSUE=Pollen; MEDLINE=9532249; PubMed=7608114;
RX Hino K., Yamamoto S., Sano O., Taniguchi Y., Kohno K., Usui M.,
RA Fukuda S., Hanazawa H., Haruyama H., Kurimoto M.;
RT Carbohydrate structures of the glycoprotein allergen Cry j 1 from
J. Biomed. 117:289-295 (1995)
CC -I PTM: CONTAINS FUCOSE/XYLose-CONTAINING N-LINKED OLIGOSACCHARIDES.
CC -I DISCRETE: THIS PROTEIN IS THE MAJOR ALLERGEN OF JAPANESE CEDAR.
CC POLLEN, THE MOST COMMON POLLEN ALLERGEN IN JAPAN.
CC -I MISCELLANEOUS: THE SEQUENCE OF CRY J 1 FORM A IS SHOWN HERE. FORM

P52420 arabidopsis
P07339 r nodq bifid
Q04487 saccharomyces
P5602 rhizobium s
P43472 pedicoccus
Q79428 oryctolagus
P74521 synechocystis
P70091 oreochromis
P37700 clostridium
P35444 rattus norvegicus
Q9nw5 hom sapiens
Q43338 agrobacteri

FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 375 AA; 40258 MW; 81CD91DP7066DBP CRC64;

Qy 73 RPWILIFSGNMNKLKLNMPLYAGKTFDGRAEVSYVHNGAKFIRRGDTI 124
 Query Match 20.0%; Score 142; DB 1; Length 375;
 Best Local Similarity 57.7%; Pred. No. 1; 7e-07;
 Matches 30; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Db 87 RSWIIFSKNLNKLKNMPLYAGKTFDGRAEVSYVHNGAKFIRRGDTI 138
 RSWIIFSKNLNKLKNMPLYAGKTFDGRAEVSYVHNGAKFIRRGDTI 138

RESULT 6
 9612_LYCES STANDARD; PRT; 404 AA.

ID 9612 LYCES STANDARD; PRT; 404 AA.
 AC P24396; DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Style development-specific protein 9612 precursor.
 GN 9612.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermato phyta; Magnoliophyta; eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX [1]
 RN 1.
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. VF36; TISSUE=Pistil;
 RX MEDLINE=9117185; PubMed=2277637;
 RA Budelier, K.A., Smith, A.G., Gasser, C.S.;
 RT "Regulation of a stylar transmitting tissue-specific gene in
 wild-type and transgenic tomato and tobacco.",
 RL Mol. Genet. 224:183-192(1990).

-!- FUNCTION: MAY HAVE A ROLE IN THE DEVELOPMENT OF THE TRANSMITTING
 TISSUE OF THE STYLE AND/OR IN THE EVENTS RELATED TO POLLINATION
 SUCH AS SOME ASPECT IN THE FACILITATION OF COMPATIBLE POLLEN TUBE
 GROWTH.

-!- SUBCELLULAR LOCATION: secreted.

-!- TISSUE SPECIFICITY: predominately found in the pistil where it is
 found in the outer five layers of the strands of transmitting
 tissue within the upper two-thirds of the style. Found at much
 lower levels in the anthers and vegetative organs.

-!- DEVELOPMENTAL STAGE: maximum levels are found during anthesis.
 -!- SIMILARITY: 54% identical to Tomato protein D59 (AC P15722)
 AND P56 (AC P15721).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL; X515193; CAA38979.1; -.
 DR PIR; S12209; S12209.
 DR InterPro; IPR002022; Amb_allergen.
 DR Pfam; PF00544; pec_lyase; 1.
 DR PRINTS; PRO0807; AMBALLERGEN.
 KW Signal.

FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 404 STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612.
 FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 404 AA; 44298 MW; B26ED9B128D8675 CRC64;

Qy 71 GRPLMLIPSGNMNKLKLNMPLYAGKTFDGRAEVSYVHNGAKFIRRGDTI 117
 Query Match 13.9%; Score 98.5; DB 1; Length 396;
 Best Local Similarity 34.7%; Pred. No. 0.006;
 Matches 26; Conservative 12; Mismatches 22; Indels 15; Gaps 3;

Db 117 QDSEPLWIFKRDMDVILQKQELMNNSYKTIORGAS---VHSGGPCI 160
 Qy 71 GRPLMLIPSGNMNKLKLNMPLYAGKTFDGRAEVSYVHNGAKFIRRGDTI 117
 Query Match 14.2%; Score 142; DB 1; Length 375;
 Best Local Similarity 57.7%; Pred. No. 1; 7e-07;
 Matches 30; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

RESULT 7
 MP1_AMBAR STANDARD; PRT; 396 AA.

ID MP1_AMBAR STANDARD; PRT; 396 AA.
 AC P27759; DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pollen allergen Amb a 1.1 precursor (Antigen B) (Antigen Amb a 1).
 OS Ambrosia artemisiifolia (Short ragweed).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermato phyta; Magnoliophyta; eudicots;
 Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
 OC Heliantheae; Ambrosia.
 OX NCBI_TaxID=4212;

RN 1.
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=pollen;
 RX MEDLINE=9109235; PubMed=1702434;
 RA Rafnar T., Griffith I.J., Kuo M.-C., Bond J.F., Rogers B.L.,
 Klapper D.G.; "Cloning of Amb a 1 (antigen E), the major allergen family of short
 ragweed pollen.", J. Biol. Chem. 266:1229-1336(1991).

RL [2]
 RN 2.
 RP SEQUENCE FROM N.A., AND VARIANTS.
 RC TISSUE=pollen;
 RX MEDLINE=92235570; PubMed=1809687;
 RA Griffith I.J., Pollock J., Klapper D.G., Rogers B.L., Nault A.K.;
 "Sequence polymorphism of Amb a 1 and Amb a 1R, the major allergens
 in Ambrosia artemisiifolia (short ragweed)."
 RT Int. Arch. Allergy Appl. Immunol. 96:296-304(1991).

CC --!- SUBUNIT: MONOMER.
 CC --!- TISSUE SPECIFICITY: POLLEN AND FLOWERS.
 CC --!- PTM: The N-terminus is blocked.
 CC --!- DISEASE: ONE OF THE MAJOR ALLERGENS OF THE RAGWEED POLLEN.
 CC --!- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
 CC --!- AMB A 1/AMB A 1/I/CY J 1 SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL; M0558; AA3265.1; -.
 DR EMBL; M0558; AA3265.1; -.
 DR PIR; A33909; A33909.
 DR PIR; A53240; A53240.
 DR InterPro; IPR002022; Amb_allergen.
 DR Pfam; PF00544; pec_lyase; 1.
 DR PRINTS; PRO0807; AMBALLERGEN.

KW Signal; Antigen; Allergen; Signal; Multigene family; Polymorphism.

FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 396 POLLEN ALLERGEN AMB A 1.1.
 FT VARIANT 92 92 E->D.
 SQ SEQUENCE 396 AA; 42709 MW; 0C87DEC92B8841D CRC64;

RESULT 8

ID	MP13_AMBAR	STANDARD;	PRT;	397 AA.				
AC	P2775;							
DT	01-AUG-1992 (Rel. 23, Created)							
DT	01-AUG-1992 (Rel. 23, Last sequence update)							
DT	16-OCT-2001 (Rel. 40, Last annotation update)							
DE	Pollen allergen Amb a 1.3 precursor (Antigen E) (Antigen Amb a I).							
OS	Ambrosia artemisiifolia (Short ragweed).							
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;							
OC	Spermatophyta; Magnoliophyta; eudicots; core eudicots;							
OC	Asteridae; easterididae II; Asterales; Asteraeae; Asteroideae;							
OX	NCBI_TaxID=4212;							
RN	11] °							
RP	SEQUENCE FROM N.A.							
RC	TISSUE=Pollen;							
RX	Medline=9109325; PubMed=1702434;							
RA	Rafnar T., Griffith I.J., Kuo M.-C., Bond J.F., Rogers B.L.,							
RA	Klapser D.G.; "Cloning of Amb a I (antigen B), the major allergen family of short							
RT	ragweed pollen"; J. Biol. Chem. 266:12229-1236(1991).							
RL	[2]							
RP	SEQUENCE FROM N.A., AND VARIANTS.							
RC	TISSUE=Pollen;							
RX	Medline=9123457; PubMed=1809687;							
RA	Griffith I.J., Pollock J., Klapser D.G., Rogers B.L., Nault A.K.; "Sequence Polymorphism of Amb a I and Amb a II, the major allergens in Ambrosia artemisiifolia (short ragweed)", Arch. Allergy Appl. Immunol. 96:296-304(1991).							
CC	-I- SUBUNIT: MONOMER.							
CC	-I- TISSUE SPECIFICITY: POLLEN AND FLOWERS.							
CC	-I- PTM: THE N-terminus is blocked							
CC	-I- DISEASE: ONE OF THE MAJOR ALLERGENS OF THE RAGWEED POLLEN.							
CC	-I- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.							
CC	AMB A 1/AMB A II/CRY J 1 SUBFAMILY.							
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).							
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).							
DR	EMBL; X67158; CAA47631.1; -.							
DR	EMBL; X67159; CAA47631.1; -.							
DR	EMBL; X67160; CAA47631.1; -.							
DR	PIR; S26211; S26211; Amb-allergen.							
DR	InterPro; IPR002022; Amb-allergen.							
DR	PRINTS; PRO00807; AMBALLERGEN.							
KW	Lyase; Signal.							
FT	SIGNAL; Signal.	1	25	POTENTIAL.				
FT	CHAIN	26	397	PECTATE LYASE.				
FT	ACT SITE	272	272	POTENTIAL.				
FT	CARBONID	134	134	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBONID	227	227	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CONFFLICT	156	156	S -> C (IN MRNA).				
FT	CONFFLICT	189	190	GS -> SG (IN MRNA).				
FT	CONFFLICT	200	200	S -> D (IN MRNA).				
FT	CONFFLICT	202	202	H -> R (IN MRNA).				
FT	CONFFLICT	249	249	H -> N (IN MRNA).				
FT	SEQUENCE	397 AA;	44351 MW;	EFO082C85DA7643F CRC64;				
Query Match	Best Local Similarity	13.1%	Score	93;	DB	1;	Length	397;
Query Match	Best Local Similarity	13.6%	Score	97;	DB	1;	Length	397;
Matches	Conservative	7;	Mismatches	17;	Indels	4;	Gaps	2;
QY	67 FTLMGRPLWTFSGMNKKKMPMYIAGYKTFDGRRAEVSYVW-NGA 114							
Db	105 YCVIQKEPLWIFGKWKIKLSELIVTSNKIDGRGFN--WAIQNGA 150							

Query Match

Best Local Similarity

Matches

QY

Db

52 WKNRIWLQ----PAKL-----GFTLMGRPLWIF 79

RESULT 10

ID	MP12_AMBAR	STANDARD;	PRT;	398 AA.
AC	P27760;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	10-OCT-2001 (Rel. 40, Last annotation update)			
DE	Pollen allergen Amb a 1.2 precursor (Antigen E)	(Antigen Amb a II).		
OS	Ambrosia artemisiifolia (Short ragweed).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicots; core eudicots;			
OC	Asteridae; eudicots II; Asterales; Asteraceae; Asteroideae;			
OC	Heリアntheae; Ambrosia.			
OX	NCBI_TaxID=4212;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Pollen;			
RX	MEDLINE-9103235; PubMed=1702434;			
RA	Krahn T., Griffith I.J., Kuo M.-C., Bond J.F., Rogers B.L.,			
RA	Klapper D.G., Pollock J., Klapffer D.G., Rogers B.L., Nault A.K.,			
RT	"Cloning of Amb a I (antigen E), the major allergen family of short			
RT	ragweed pollen.";			
RL	J. Biol. Chem. 266:1229-1226(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND VARIANTS.			
RX	TISSUE=Pollen;			
RX	MEDLINE-92234570; PubMed=1609687;			
RA	Griffith I.J., Pollock J., Klapffer D.G., Rogers B.L., Nault A.K.,			
RA	in Ambrosia artemisiifolia (short ragweed).";			
RT	Int. Arch. Allergy Appl. Immunol. 96:296-304(1991).			
RL	--!- SUBUNIT: MONOMER.			
CC	--!- TISSUE SPECIFICITY: POLLEN AND FLOWERS.			
CC	--!- PTM: The N-terminus is blocked.			
CC	--!- DISEASE: ONE OF THE MAJOR ALLERGENS OF THE RAGWEED POLLEN.			
CC	--!- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.			
CC	AMB A I/AMB A II/CRY J I SUBFAMILY.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC				
DR	EMBL; M02981; AAA22666.1; --.			
DR	PIR; B30909; B30999.			
DR	InterPro; IPR002022; Amb_allergen.			
DR	Pfam; PF00544; pec_lyase_1.			
DR	PRINTS; PR00807; AMBALLERGEN.			
KW	Allergen; Allergen; Signal; Multigene family; Polymorphism.			
FT	SIGNAL 1 25 POTENTIAL.			
FT	CHAIN 26 398 POLLEN ALLERGEN AMB A 1.2.			
FT	VARIANT 345 345 R -> K.			
FT	VARIANT 381 381 L -> I.			
SQ	SEQUENCE 398 AA; 43664 MW; 020DC662D9B7416C CRC64;			
Query Match	13.1%; Score 93; DB 1; Length 398;			
Best Local Similarity	30.5%; Pred. No. 0.022; Matches 32; Conservative 5; Mismatches 34; Indels 34; Gaps 3;			
Qy	52 WKNRIRWLO-----FAKUT-----GFTLMGRPWIIP 79			
Db	62 WANRQALADACQAFAKTYGGHDVYTVNSDKDDVANPKRGTAAQNPLWII 121			
Qy	80 SGMMNIKUKPMVITAGYKTFDGRERAESVYHNGAKIRRVIDI 124			
Db	122 KRNVVIHQELQYLVNSDKTIDGRGVKVN--VAGLITLMVGNV 164			
RESULT 11	MPA2_AMBAR	STANDARD;	PRT;	397 AA.
ID	MPA2_AMBAR			
AC	P27762;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Pollen allergen Amb a 2 precursor (Antigen K) (Antigen Amb a II).			
OS	Ambrosia artemisiifolia (Short ragweed).			
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicots; core eudicots;			
OC	Asteridae; eudicots II; Asterales; Asteraceae; Asteroideae;			
OC	Heliantheae; Ambrosia.			
OX	NCBI_TaxID=4212;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Flower;			
RX	MEDLINE-92013060; PubMed=1717566;			
RA	Roger B.L., Morgenstern J.P., Griffith I.J., Yu X.-B.,			
RA	Counsell C.M., Brauer A.W., King T.P., Garman R.D., Kuo M.-C.C.,			
RT	"Complete sequence of the allergen Amb alpha II. Recombinant expression and reactivity with T cells from ragweed allergic patients";			
RT	J. Immunol. 147:2547-2552(1991).			
RL				
RN	[2]			
RP	SEQUENCE FROM N.A., AND VARIANTS.			
RC	TISSUE=Pollen;			
RX	MEDLINE-92234570; PubMed=1609687;			
RA	Griffith I.J., Pollock J., Klapffer D.G., Rogers B.L., Nault A.K.,			
RA	in Ambrosia artemisiifolia (short ragweed).";			
RT	Int. Arch. Allergy Appl. Immunol. 96:296-304(1991).			
RL	--!- SUBUNIT: MONOMER.			
CC	--!- TISSUE SPECIFICITY: POLLEN AND FLOWERS.			
CC	--!- PTM: The N-terminus is blocked.			
CC	--!- DISEASE: ONE OF THE MAJOR ALLERGENS OF THE RAGWEED POLLEN.			
CC	--!- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1..			
CC	AMB A I/AMB A II/CRY J I SUBFAMILY.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC				
DR	EMBL; MB0561; AAA22671.1; --.			
DR	PIR; A46469; A46469.			
DR	InterPro; IPR002022; Amb_allergen.			
DR	Pfam; PF00544; pec_lyase_1.			
DR	PRINTS; PR00807; AMBALLERGEN.			
KW	Antigen; Allergen; Signal; Polymorphism.			
FT	SIGNAL 1 25 POTENTIAL.			
FT	CHAIN 26 397 POLLEN ALLERGEN AMB A 2.			
FT	VARIANT 70 70 N -> D (DETECTED ONLY IN FLOWER DNA).			
FT	VARIANT 138 138 K -> T (DETECTED ONLY IN FLOWER DNA).			
FT	VARIANT 321 321 K -> R (DETECTED ONLY IN FLOWER DNA).			
SQ	SEQUENCE 397 AA; 44082 MW; C78617E4CB43D1D CRC64;			
Query Match	12.9%; Score 92; DB 1; Length 397;			
Best Local Similarity	42.3%; Pred. No. 0.028; Matches 22; Conservative 7; Mismatches 21; Indels 2; Gaps 1;			
Qy	73 RPFLWIFSGMMNIKUKPMVITAGYKTFDGRERAESVYHNGAKIRRVIDI 124			
Db	114 RPFLWIFFORMYLQENVMVWSDKTIDGRGAKVELV--SGITLMVGNV 163			
RESULT 12	PE56_LYCES	STANDARD;	PRT;	398 AA.
ID	PE56_LYCES			
AC	P15721;			

DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE probable pectate lyase P56 precursor (EC 4.2.2.2).
 GN LAT56.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 NCBI_TaxID=4001;
 RN [1]
 RP SUBSEQUENCE FROM N.A.
 RC STRAIN=cv. VF35; TISSUE=Anther;
 RX MEDLINE=91122485; PubMed=198319;
 RA Wing R.A.; Yamaguchi J.; Larabell S.K.; Ursin V.M.; McCormick S.;
 RA "Molecular and genetic characterization of two pollen-expressed genes
 RT that have sequence similarity to pectate lyases of the plant pathogen
 RT Erwinia";
 RL Plant Mol. Biol. 14:17-28(1990).
 RN [2]
 RP STRAIN=cv. VF35; TISSUE=Anther;
 RC Wing R.A.;
 RA Submitted (SPP=1994) to the EMBL/GenBank/DDBJ databases.
 RL GROWTH.
 CC -!- CATALYTIC ACTIVITY: Eliminative cleavage of pectate to give
 CC oligosaccharides with 4-deoxy-alpha-D-gluc-4-enuronosyl groups at
 CC their non-reducing ends.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ANTERS AND POLLEN.
 CC -!- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
 CC -!- FUNCTION: MIGHT BE NEEDED DURING POLLEN DEVELOPMENT AND TUBE
 CC REVISIONS.
 CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial/
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; MS0562; AA032670; 1.
 CC DR PIR; D53240; DS3240.
 CC DR InterPro; IPR02022; Amb_allergen.
 CC DR PR00544; pec_lyse; 1.
 CC DR PRINTS; PR00807; AMBALLERGEN.
 CC KW Allergen; Signal; Multigene Family; Polymorphism.
 CC FT SIGNAL 1 25 POTENTIAL.
 CC FT CHAIN 26 392 POLLEN ALLERGEN AMB A 1.4.
 CC FT VARIANT 182 188 SHDGPPV->CGDGPAA.
 CC SQ SEQUENCE 392 AA; 42442 MW; TB619C12F365DA9 CRC64;
 CC -----
 CC Query Match 73 RPLWITFSGNNTIKLMPMYIAGYKTFGRRAEVSYVHNGAKFIRYDII 124
 CC Best Local Similarity 44.2%; Pred. No. 0.058; Mismatches 20; Indels 2; Gaps 1;
 CC Matches 23; Conservative 7; MisMatches 7; InDel 2; Gap 1;
 DB 114 RPLWITFARDMVRILDRELAINNDKTIDGRGAKWEINAGFA-IIVWKII 163
 CC -----
 RESULT 14
 PEL_LILLO STANDARD; PRT; 434 AA.
 ID PEL_LILLO
 AC P40973;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE pectate lyase precursor (EC 4.2.2.2).
 OS Lilium longiflorum (Trumpet lily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
 OC Lilium.
 OX NCBI_TaxID=4690;
 RN [1]
 RP SUBSEQUENCE FROM N.A.
 RC STRAIN=cv. Nellie white; TISSUE=Pollens;
 RA Kim S.R.; Finkel D.J.; An G.;
 RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
 CC -!- CATALYTIC ACTIVITY: Eliminative cleavage of pectate to give
 CC oligosaccharides with 4-deoxy-alpha-D-gluc-4-enuronosyl groups at
 CC their non-reducing ends.
 CC -!- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial/
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
 OC Heisantheae; Ambrosia.
 OX NCBI_TaxID=41212;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANTS.
 RC TISSUE=Pollens;
 RX MEDLINE=92234570; PubMed=1809687;
 RA Griffith J.J.; Pollock J.; Klapser D.G.; Rogers B.L.; Nault A.K.;
 RT Spermatophyta polymorphism of Amb a I and Amb a II, the major allergens
 RT in Ambrosia artemisiifolia (short ragweed)",
 RL Int. Arch. Allergy Appl. Immunol. 96:296-304(1991).
 CC -!- SUBUNIT: MONOMER.
 CC -!- TISSUE SPECIFICITY: POLLEN AND FLOWERS.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- DISEASE: ONE OF THE MAJOR ALLERGENS OF THE RAGWEED POLLEN.
 CC -!- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
 CC AMB A IAMB A II/GY J I SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial/
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; MS0562; AA032670; 1.
 CC DR PIR; D53240; DS3240.
 CC DR InterPro; IPR02022; Amb_allergen.
 CC DR PR00544; pec_lyse; 1.
 CC DR PRINTS; PR00807; AMBALLERGEN.
 CC KW Allergen; Signal; Multigene Family; Polymorphism.
 CC FT SIGNAL 1 25 POTENTIAL.
 CC FT CHAIN 26 392 POLLEN ALLERGEN AMB A 1.4.
 CC FT VARIANT 182 188 SHDGPPV->CGDGPAA.
 CC SQ SEQUENCE 392 AA; 42442 MW; TB619C12F365DA9 CRC64;
 CC -----
 CC Query Match 73 RPLWITFSGNNTIKLMPMYIAGYKTFGRRAEVSYVHNGAKFIRYDII 124
 CC Best Local Similarity 44.2%; Pred. No. 0.058; Mismatches 20; Indels 2; Gaps 1;
 CC Matches 23; Conservative 7; MisMatches 7; InDel 2; Gap 1;
 DB 114 RPLWITFARDMVRILDRELAINNDKTIDGRGAKWEINAGFA-IIVWKII 163
 CC -----
 RESULT 15
 PEL_LILLO STANDARD; PRT; 434 AA.
 ID PEL_LILLO
 AC P40973;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE pectate lyase precursor (EC 4.2.2.2).
 OS Lilium longiflorum (Trumpet lily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
 OC Lilium.
 OX NCBI_TaxID=4690;
 RN [1]
 RP SUBSEQUENCE FROM N.A.
 RC STRAIN=cv. Nellie white; TISSUE=Pollens;
 RA Kim S.R.; Finkel D.J.; An G.;
 RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
 CC -!- CATALYTIC ACTIVITY: Eliminative cleavage of pectate to give
 CC oligosaccharides with 4-deoxy-alpha-D-gluc-4-enuronosyl groups at
 CC their non-reducing ends.
 CC -!- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial/
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sb-sib.ch).

CC EMBL; ZU7328; CAA8976_1; -.

CC PIR; S22612; S22612; -.

DR InterPro; IPR02022; Amb_allergen.

DR Pfam; PF00544; pec_lyase_1.

DR PRINTS; PRO0807; AMBALERGEN.

KW Lyase, signal.

FT SIGNAL, 1 22 POTENTIAL.

FT CHAIN 23 449 PROBABLE PECTATE LYASE P59.

FT ACT_SITE 325 325 POTENTIAL.

FT CARBOHYD 56 56 N-LINKED (GICNAC. . .) (POTENTIAL).

FT CARBOHYD 80 80 N-LINKED (GICNAC. . .) (POTENTIAL).

FT CARBOHYD 81 81 N-LINKED (GICNAC. . .) (POTENTIAL).

FT SEQUENCE 449 AA; 50893 MW; 17E3AA13F173B03C CRC64;

Query Match 11.6%; Score 82.5; DB 1; Length 449;

Best Local Similarity 55.9%; Pred. No. 0.064; DB 1;

Matches 19; Conservative 3; Mismatches 12; Indels 75; Gaps 7.

FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SEQUENCE 434 AA; 48457 MW; C1F3E30AD2BBDD64 CRC64;

QY 151 RPLWIFIGKSMVIRLKQBLIINNDKTIDRGANV 184

Db 102 IDKCWRCDPWADNKKLAKCAMGFSKAIGKGKQEFYVVDNSDDNDPKPGILRHAVI 161

QY 72 -RRPMLIIFSGMNNTKLKMMVYAGKTFGRRAEVSVYHV-NCA---KFIRV 120

Db 162 QKEPLWIIFKRGMNIRLHQEMIMOSDKTIDARGVN--VHITKGAGITLQYIKVW 213

Result 15

PB59_LYCES

ID PB59_LYCES STANDARD; PRT; 449 AA.

AC P15722; 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Probable pectate lyase P59 precursor (EC 4.2.2.2).

GN LAT59.

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eudicots I; Solanales; Solanaceae; Solanum. [1]

RN SEQUENCE FROM N-A.

RP STRAIN-CV: VF36; TISSUE=Anther;

RX MEDLINE=91122485; PubMed=1983191;

RA Wing, R.A.; Yamaguchi, J.; Larabell, S.K.; Ursin, V.M.; McCormick, S.; McCormick, S.; RT "Molecular and genetic characterization of two pollen-expressed genes that have sequence similarity to pectate lyases of the plant pathogen Erwinia"; RT Erwinia"; Plant Mol. Biol., 14:17-28(1990).

RL - FUNCTION: MIGHT BE NEEDED DURING POLLEN DEVELOPMENT AND TUBE GROWTH.

CC -!- CATALYTIC ACTIVITY: Eliminative cleavage of pectate to give CC oligosaccharides with 4-deoxy-alpha-D-gluc-4-enuronosyl groups at CC their non-reducing ends.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN ANHERS AND POLLEN.

CC -!- SIMILARITY: BELONGS TO THE POLISACCHARIDE LYASE FAMILY 1.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sb-sib.ch).

CC EMBL; X15499; CAA3323_1; -.

DR PIR; S227098; S227098.

DR InterPro; IPR002022; Amb_allergen.

DR Pfam; PF00544; pec_lyase_1.

DR PRINTS; PRO0807; AMBALERGEN.

KW Lyase; Multigene family; Signal.

FT SIGNAL, 1 22 POTENTIAL.

OM protein - protein search, using SW model
Run on: May 5, 2003, 16:54:26 ; Search time 84 Seconds
(without alignments)
32.694 Million cell updates/sec

Title: US-09-142-524D-3
Perfect score: 711
Sequence: 1 MKVTVAFFNQFGPNRRVFIKR.....KFIRRVGDITAAAYQNPASWK 134
Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBI_21:
1: sp_archea;*
2: sp_bacteria;*
3: sp_fungi;*
4: sp_human;*
5: sp_invertebrate;*
6: sp_mammal;*
7: sp_micr;*
8: sp_organelle;*
9: sp_plage;*
10: sp_plant;*
11: sp_reptile;*
12: sp_virus;*
13: sp_vertebrate;*
14: sp_unclassified;*
15: sp_rvirus;*
16: sp_bacteriap;*
17: sp_archeap;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	188	26.4	374	0BRUR1
2	150	21.1	367	0QLIT2
3	150	21.1	367	0QLIT1
4	150	21.1	367	0QM4S6
5	150	21.1	367	0QM4S4
6	150	21.1	367	0QM4S3
7	150	21.1	367	0QM4S2
8	150	21.1	367	0QM4X51
9	146	20.5	367	0QM4S5
10	144	20.3	367	0Q3XL6
11	110.5	15.5	367	0Q3Z04
12	110.5	15.5	542	0Q8V40
13	107.5	15.1	507	0QFY19
14	104.5	14.7	463	0Q8SCP2
15	100.5	14.1	453	0Q8ALR5
99	13.9	10	472	0Q9LFP5

17 97 13.6 455 10 064510
18 95.5 13.4 181 10 023666
19 95.5 13.4 410 10 0Q9FMK5
20 95.5 13.4 432 10 0Q93Z25
21 95.5 13.4 459 10 023665
22 95.5 13.4 459 10 0Q9MS2
23 95 13.4 392 10 0Q9FM66
24 95 13.4 452 10 0Q9LRM5
25 94.5 13.3 226 10 023667
26 94.5 13.3 354 10 0Q94Q01
27 94.5 13.3 398 10 0Q9M505
28 94.5 13.3 404 10 0Q9SB71
29 94.5 13.3 408 10 0Q9C5MB
30 94.5 13.3 431 10 023017
31 93.5 13.2 392 10 0Q9FXD8
32 93.5 13.2 407 10 0Q9SDW4
33 93.5 13.2 408 10 0Q8W116
34 93 13.1 450 10 040319
35 91.5 12.9 368 10 0Q9C8G4
36 90.5 12.7 409 10 0Q93XJ1
37 90 12.7 409 10 0Q9LTZ0
38 89.5 12.6 324 10 0Q8S345
39 89.5 12.6 398 10 0Q4783
40 88.5 12.4 297 10 0Q9FY87
41 88 12.4 438 10 0Q43862
42 87 12.2 368 10 0Q9LFT5
43 85.5 12.0 416 10 0Q9M828
44 85 12.0 227 10 0Q23668
45 84.5 11.9 401 10 024554

ALIGNMENTS

RESULT 1
QBRUR1
TD QBRUR1 PRELIMINARY; PRT; 374 AA.
AC OBRUR1;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE CRY J 1 precursor: 11
GN CRY J 1.1 OR CRY J 1.2.
OS CRYPTOMERIA JAPONICA (Japanese cedar).
OC Eukaryota; Viriplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Cryptomeria.
OX NCBI_TaxID=3369;
RN SEQUENCE FROM N.A.
RP TISSUE=POLENN;
RC Putamura N., Shinohara K.;
RT "Isolation and characterization of cDNAs encoding major allergen Cry J 1 from Cryptomeria japonica pollen.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB081309; BAB86286.1; --.
DR EMBL; AB081310; BAB86287.1; --.
KW Signal. 1 21 POTENTIAL.
FT SIGNAL 1 21
FT CHAIN 22 374 CRY J 1.
SQ SEQUENCE 374 AA; 40720 MW; 90D0085D24B2BD4 CRC64;

Query Match 26.4%; Score 188; DB 10; Length 374;
Best Local Similarity 71.2%; Pred. No. 2 6e-12; Indels 0; Gaps 0;
Matches 37; Conservative 4; Mismatches 11;

QY 73 RPIWIIIFSGNMNLKQPMYIGKTFGRDGRAEVSVYHVNKAKFIRRVGDIT 124
Db 87 RPLWIIIFSGNMNLKQPMYIGKTFGRDGRAEVSVYHVNKAKFIRRVGDIT 138

RESULT 2
Q9LIT2 PRELIMINARY; PRT; 367 AA.

AC Q9M4S6
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE Pollen major allergen 1-2.
 OS Juniperus virginiana (Eastern red cedar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytina; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
 OC NCBI_TaxID=39584;
 RN [1]_SEQUENCE FROM N.A.
 RX MEDLINE=21315424; PubMed=11422137;
 RA Midoro-Horii T.M., Goldblum R.M., Brooks E.G.;
 RT "Identification of mutations in the genes for the pollen allergens of
 eastern red cedar (Juniperus virginiana).";
 RL Clin. Exp. Allergy 31:771-778(2001).
 EMBL; AF15427; AAF8064..;
 DR InterPro; IPR002022; Amb_allergen.
 DR Pfam; PF00544; pec_lyase_1.
 DR PRINTS; PR00807; AMBALERGEN.
 SQ 73 RPWIFISGNNNIKLKKMPMYIAGYKTFDGRRAEVSVYHNGAKFIRRVDGII 124
 Query Match : ||||||| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Best Local Similarity 55.8%; Pred. No. 3.7e-08; Length 367;
 Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 DR PRINTS; PR00807; AMBALERGEN.
 SQ 87 KTWIILFSQNNNIKLKKMPLYVAGHKTIDGRGADVHLGLNGGPCFLFRKVSHI 138
 Query Match : ||||||| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Best Local Similarity 55.8%; Pred. No. 3.7e-08; Length 367;
 Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 DR PRINTS; PR00807; AMBALERGEN.

RESULT 3
 OQLT1 PRELIMINARY; PRT; 367 AA.
 ID Oqlt1 ; PRELIMINARY; PRT; 367 AA.
 AC Oqlt1 ; PRELIMINARY; PRT; 367 AA.
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE Pollen major allergen 1-1.
 OS Juniperus virginiana (Eastern red cedar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytina; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
 OC NCBI_TaxID=39584;
 RN [1]_SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21315424; PubMed=11422137;
 RA Midoro-Horii T.M., Goldblum R.M., Brooks E.G.;
 RT "Identification of mutations in the genes for the pollen allergens of
 eastern red cedar (Juniperus virginiana).";
 RL Clin. Exp. Allergy 31:771-778(2001).
 EMBL; AF15429; AAF80166..;
 DR InterPro; IPR002022; Amb_allergen.
 DR Pfam; PF00544; pec_lyase_1.
 DR PRINTS; PR00807; AMBALERGEN.
 SQ SEQUENCE 367 AA; 39768 MW; DCBD1981A74E4711 CRC64;
 Query Match 21.1%; Score 150; DB 10; Length 367;
 Best Local Similarity 55.8%; Pred. No. 3.7e-08;
 Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 DR PRINTS; PR00807; AMBALERGEN.

RESULT 4
 Q9M4S6 PRELIMINARY; PRT; 367 AA.
 ID Q9M4S6
 AC Q9M4S6
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE Cup s 1 pollen allergen.

Query Match 73 RPWIFISGNNNIKLKKMPMYIAGYKTFDGRRAEVSVYHNGAKFIRRVDGII 124
 Best Local Similarity 55.8%; Pred. No. 3.7e-08; Length 367;
 Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 DR PRINTS; PR00807; AMBALERGEN.

RESULT 5
 Q9M4S4 PRELIMINARY; PRT; 367 AA.
 ID Q9M4S4
 AC Q9M4S4
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DR Cup s 1 pollen allergen.
 OS Cupressus semperfervirens.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytina; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
 OC NCBI_TaxID=13469;
 RN [1]_SEQUENCE FROM N.A.
 RA Monsalve R.I., Vilalba M., Rodriguez R.;
 RT "Cloning and expression of Cup s 1, the major allergen of the pollen
 of Cupressus semperfervirens.,"
 RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF237493; AAF26271..;
 DR InterPro; IPR002022; Amb_allergen.
 DR Pfam; PF00544; pec_lyase_1.
 DR PRINTS; PR00807; AMBALERGEN.
 SQ SEQUENCE 367 AA; 39934 MW; 974D3011D74E3D6E CRC64;
 Query Match 21.1%; Score 150; DB 10; Length 367;
 Best Local Similarity 55.8%; Pred. No. 3.7e-08;
 Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 DR PRINTS; PR00807; AMBALERGEN.

RESULT 6
 Q9M4S3 PRELIMINARY; PRT; 367 AA.
 ID Q9M4S3
 AC Q9M4S3
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DR Cup s 1 pollen allergen.
 OS Cupressus sempervirens.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytina; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
 OC NCBI_TaxID=13469;

RN [1] SEQUENCE FROM N.A.
 RP Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 RA Monsalve R.I.; Villalba M.; Rodriguez R.; major allergen of the pollen
 RT "Cloning and expression of Cup s 1, the major allergen of the pollen
 of *Cupressus sempervirens*."
 RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF257494; AACF2628.1; -.
 DR InterPro; IPR002022; Amb_allergen.
 DR Pfam; PF0054; pec_lyase_1.
 DR PRINTS; PR00807; AMBALLERGEN.
 SQ SEQUENCE 367 AA; 39832 MW; B5DFBF5A61C07A53 CRC64;
 Query Match 21.1%; Score 150; DB 10; Length 367;
 Best Local Similarity 55.8%; Pred. No. 3.7e-08;
 Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 PRT: 367 AA.

QY 73 RPLWLTFSGNMNIKUKMPVYAGKTFDGRRAEVSVYHNGAKFIRRVDGII 124
 DB 87 KALWIIFSQNNMIKUKMPVYAGKTFDGRADGVHLGNGGCPCLFMRKVSHVI 138

RESULT 7
 Q9M4S2 PRELIMINARY; PRT: 367 AA.
 ID Q9M4S2
 AC Q9M4S2; (T-TREMBLrel. 15, Created)
 DT 01-OCT-2000 (T-TREMBLrel. 15, last sequence update)
 DT 01-OCT-2000 (T-TREMBLrel. 15, last annotation update)
 DT 01-JUN-2002 (T-TREMBLrel. 21, last annotation update)
 DE Cup s 1 pollen allergen.
 GN CUPSI.
 OS *Cupressus sempervirens*.
 OC Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
 OC NCBI_TaxID=13469;
 RN [1] SEQUENCE FROM N.A.
 RP Monsalve R.I., Villalba M.; Rodriguez R.; major allergen of the pollen
 RA "Cloning and expression of Cup s 1, the major allergen of the pollen
 of *Cupressus sempervirens*."
 RT Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AF257495; AACF2629.1; -.
 DR InterPro; IPR002022; Amb_allergen.
 DR Pfam; PF0054; pec_lyase_1.
 DR PRINTS; PR00807; AMBALLERGEN.
 SQ SEQUENCE 367 AA; 39819 MW; A87E055A61C07A53 CRC64;
 Query Match 21.1%; Score 150; DB 10; Length 367;
 Best Local Similarity 55.8%; Pred. No. 3.7e-08;
 Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

RESULT 8
 Q3X51 PRELIMINARY; PRT: 367 AA.
 ID Q3X51
 AC Q3X51;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Putative allergen Cup a 1.
 GN JUN O 1.
 OS *Juniperus oxycedrus* (Prickly juniper).
 OC Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Juniperus.
 OC NCBI_TaxID=69008;
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE=POLEN;
 RA Lacovacci P.; Di Felice G.; Pini C.;
 RA "Cloning of *Juniperus oxycedrus* major allergen.";
 SQ SEQUENCE 367 AA; 39809 MW; AFF976042A9F28 CRC64;

RESULT 9
 Q9M4S5 PRELIMINARY; PRT: 367 AA.
 ID Q9M4S5
 AC Q9M4S5; (T-TREMBLrel. 15, Created)
 DT 01-OCT-2000 (T-TREMBLrel. 15, last sequence update)
 DT 01-OCT-2000 (T-TREMBLrel. 15, last annotation update)
 DT 01-JUN-2002 (T-TREMBLrel. 21, last annotation update)
 DE Cup s 1 pollen allergen.
 GN CUPSI.
 OS *Cupressus sempervirens*.
 OC Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
 OC NCBI_TaxID=13469;
 RN [1] SEQUENCE FROM N.A.
 RP Monsalve R.I., Villalba M.; Rodriguez R.; major allergen of the pollen
 RA "Cloning and expression of Cup s 1, the major allergen of the pollen
 of *Cupressus sempervirens*."
 RT Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AF257492; AACF2626.1; -.
 DR InterPro; IPR002022; Amb_allergen.
 DR Pfam; PF0054; pec_lyase_1.
 DR PRINTS; PR00807; AMBALLERGEN.
 SQ SEQUENCE 367 AA; 39894 MW; 5D56FC0E3263B741 CRC64;
 Query Match 20.5%; Score 146; DB 10; Length 367;
 Best Local Similarity 53.8%; Pred. No. 1e-07;
 Matches 28; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

RESULT 10
 Q93X16 PRELIMINARY; PRT: 367 AA.
 ID Q93X16
 AC Q93X16;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DR Putative allergen Cup a 1 precursor.
 GN CUP A 1.
 OS *Cupressus arizonica*.
 OC Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
 OC NCBI_TaxID=49011;
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE=POLEN;
 RA Butteroni C.; Di Felice G.; Pini C.;
 RA "Cloning of *Cupressus Arizonica* major allergen.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ278498; CAIC37790.2; -.
 DR Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 367 PUTATIVE ALLERGEN CUP A 1.
 SQ SEQUENCE 367 AA; 39809 MW; AFF976042A9F28 CRC64;

Query Match^{*} 20.3%; Score 144; DB 10; Length 367;
 Best Local Similarity 53.8%; Pred. No. 1.7e-07; OS
 Matches 28; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 73 RPHWITFGNMINIKLKMMPYIAGKTFGRRAEVSYVHNGAKFIRVDGII 124
 Db 87 KALWIFISQNMINIKLQMPLYAVGYKTIDGRGADVHLGNGGPFCLMRTASHVI 138

RESULT 11

Q33Z04 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 ID Q33Z04 PRELIMINARY; PRT; 501 AA.
 AC 093Z04; DT 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)
 DE AT395422/F28P10_100 (Putative pectate lyase).
 GN AR3G5420.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OK NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Koescena E., Meyers M.C.,
 RA Bath J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones".
 RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Bath J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamoto Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene At3g5420 (GI:15233132)".
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY058870; AAC042571; -.
 DR EMBL; AY074331; AAC070271; -.
 DR InterPro; IPR002022; Amb_allergen.
 DR Pfam; PF00544; pec_lyase; 1.
 KW Lyase.
 SQ SEQUENCE 501 AA; 5329 MW; 9E0DE36DBF4C7ABB CRC64;
 Query Match 15.5%; Score 110.5; DB 10; Length 501;
 Best Local Similarity 43.3%; Pred. No. 0.0011; OS
 Matches 26; Conservative 9; Mismatches 20; Indels 5; Gaps 2;

QY 67 FTMGRPLWIFSGNMINIKLKMMPYIAGKTFGRRAEVSYVHNGAKFIRVDGII 124
 Db 139 YGVIOEPLWIVFSSNMLRKLQELINTSYKTLDRG--SAVHLTGNCLTQYQHII 195

RESULT 12

Q9SY40 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 ID Q9SY40 PRELIMINARY; PRT; 542 AA.
 AC 09SY40; DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-JUN-2001 (TREMBrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBrel. 17, Last annotation update)
 DE F28P10_100.

Query Match 20.3%; Score 144; DB 10; Length 367;
 Best Local Similarity 53.8%; Pred. No. 1.7e-07; OS
 Matches 28; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 31 IDIFASKRFLQLQKNTIGTRRNKRNLQFAKLTGFTLGRPLWIFSGNMINIKLMPYIAGKTFGRRAEVSYVHNGAKFIRVDGII 124
 Db 237 IDIFASKRFLQLQKNTIGTRRNKRNLQFAKLTGFTLGRPLWIFSGNMINIKLMPYIAGKTFGRRAEVSYVHNGAKFIRVDGII 195

SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL049655; CAB41092.; -.
 DR InterPro; IPR002022; Amb_allergen.
 DR Pfam; PF00544; pec_lyase; 1.
 DR PRINTS; PRO0807; AMBALLERGEN.
 KW Lyase.
 SQ SEQUENCE 542 AA; 58573 MW; EB379D613B72347 CRC64;
 Query Match 15.5%; Score 110.5; DB 10; Length 542;
 Best Local Similarity 43.3%; Pred. No. 0.013; OS
 Matches 26; Conservative 9; Mismatches 20; Indels 5; Gaps 2;

Q9FY19 :|||||:|||||:|||||:|||||:
 ID Q9FY19 PRELIMINARY; PRT; 507 AA.
 AC 09FY19; DT 01-MAR-2001 (TREMBrel. 16, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DR Polien major allergen 2 protein precursor.
 GN JNA2.
 OS Juniperus ashei (Ozark white cedar).
 OC Juniperata; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Juniperus.
 OK NCBI_TaxID=13101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-MALE POLLEN;
 RX MEDLINE=20013896; PubMed=10944464;
 RA Yokoyama M., Miyahara M., Shinizu K., Kino K., Tsuno H.;
 RT Purification, Identification and cDNA cloning of Jun a 2, the second
 RT major allergen of mountain cedar pollen.;
 RL Biochem. Biophys. Res. Commun. 275:195-202(2000).
 CC - SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES.
 CC (POLYGLACTURONASES).
 DR EMBL; AJ404653; CAC05582.1; -.
 DR HSSP; P26509; 1BHE.
 DR InterPro; IPR000743; GH28.
 DR InterPro; IPR000408; Reg chr condens.
 DR Pfam; PF00295; Glyco_hydro_207; 1.
 DR PROSITE; PS00502; POLYGLACTURONASE; UNKNOWN_1.
 DR PROSITE; PS00626; RCC1_2; UNKNOWN_1.
 KW PROSITE; PS00626; RCC1_2; UNKNOWN_1.
 KW Cell wall; Glycosidase; Hydrolase; Signal.
 FT SIGNAL_1
 SQ SEQUENCE 507 AA; 55730 MW; 2B2E0AA5E958F5EA CRC64;
 Query Match 15.1%; Score 107.5; DB 10; Length 507;
 Best Local Similarity 32.3%; Pred. No. 0.0025; OS
 Matches 32; Conservative 13; Mismatches 25; Indels 29; Gaps 2;

QY 31 IDIFASKRFLQLQKNTIGTRRNKRNLQFAKLTGFTLGRPLWIFSGNMINIKLMPYIAGKTFGRRAEVSYVHNGAKFIRVDGII 90
 Db 237 IDIFASKRFLQLQKNTIGTRRNKRNLQFAKLTGFTLGRPLWIFSGNMINIKLMPYIAGKTFGRRAEVSYVHNGAKFIRVDGII 273

Query 91 MYIACKYKTFDG-----RRAEVSYVHNGAKFIRRVDGII 123
 ID :|||:|:|||:|||:|||:|||:
 AC 09SCP2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Pectate lyase-like protein.
 GN T4D2_120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae;
 OC eurosids II; Brassidales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nakamura G., Färtmann B., Dauner D., Sterr W., Holland R., Quetier F.,
 RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,
 RA Salancikat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DDJB databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Arabidopsis sequencing project;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDJB databases.
 DR EMBL; All12958; CAB64222.1; --.
 DR InterPro; IPR002022; Amb_allergen.
 DR Pfam; PF00544; Dec_lyase; 1.
 DR PRINTS; PRO0807; AMBALERGEN.
 KW lyase.
 SQ SEQUENCE 463 AA; 51225 MW; 3424B0DE4ADBA604 CRC64;

Query Match 14.1%; Score 100.5; DB 10; Length 453;
 Best Local Similarity 48.8%; Pred. No. 0.013; Mismatches 13; Indels 1; Gaps 1;
 Matches 20; Conservative 7; Gaps 1; Gaps 1;
 Sequence 453 AA; 48005 MW; 1411BEBA40901DC CRC64;

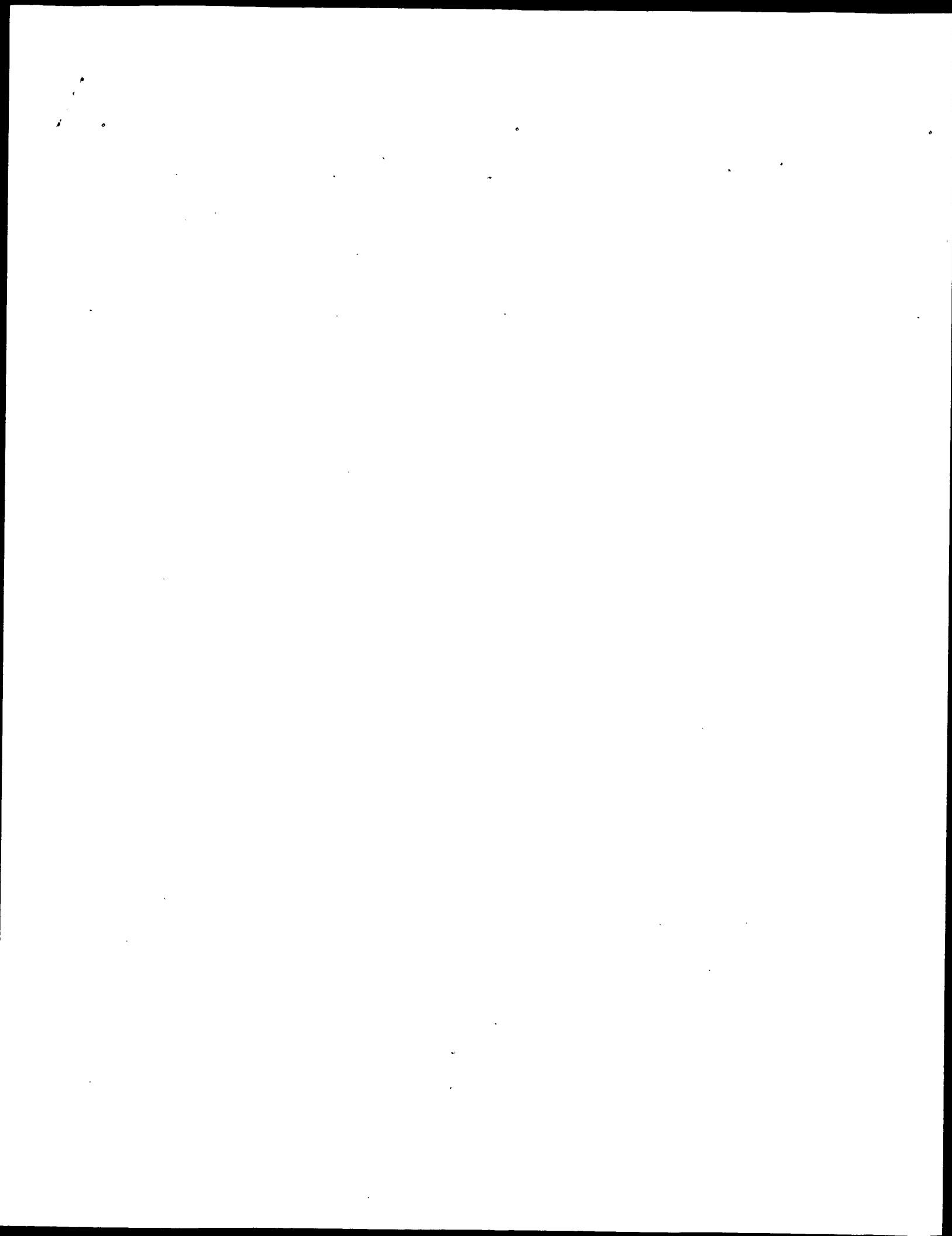
Query Match 14.1%; Score 100.5; DB 10; Length 453;
 Best Local Similarity 48.8%; Pred. No. 0.013; Mismatches 13; Indels 1; Gaps 1;
 Matches 20; Conservative 7; Mismatches 13; Indels 1; Gaps 1;
 Sequence 453 AA; 48005 MW; 1411BEBA40901DC CRC64;

Query 74 PIWITFSGNMNMKLKNPMLTAGYKUPFDGRRAEVSYVHNGA 114
 ID :|||:|||:|||:|||:|||:|||:|||:|||:
 DR 140 PIWIVAGDMTRLMELLYNYSKTIDGRANV-HVGAGGA 179

Search completed: May 5, 2003, 16:59:01
 Job time : 90 secs

RESULT 15

Q4LR5 PRELIMINARY; PRT; 453 AA.
 ID Q94LR5
 AC Q94LR5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Putative pectate lyase.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoidae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_NIPPONRARE;
 RA Buel C.R., Yuan O., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
 RA Bremer M., Burgess M., Haneke M., Shvartsbeyn M., Tsitrin T.,
 RA Riggs F., Hsiao J., Zissmann V., Blunt S., Pai G., Vanaken S.E.,
 RA Utterback T.R., Feilدبlyum T.V., Quackenbush J., Salzberg S.L.,
 RA White O., Fraser C.M.,
 RT "Oryza sativa chromosome 10 BAC OSJNB0011A08 genomic sequence.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDJB databases.
 EMBL; AC034256; ARK54283.1; -.



GenCore version 5.1.4_P5_478
 Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:48:05 ; search time 46 Seconds
 (without alignments)
 388.165 Million cell updates/sec

Title: US_09-142-524D-3

Perfect score: 711
 Sequence: 1 MKVTVAERNQFGPNRRVFIKR..... KFIRRVDDGIAYAQNPASWK 134

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext: 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : A_Geneset_101002;*

- 1: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1980.DAT:*
- 2: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1982.DAT:*
- 3: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1983.DAT:*
- 4: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1984.DAT:*
- 5: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1985.DAT:*
- 6: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1986.DAT:*
- 7: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1987.DAT:*
- 8: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1988.DAT:*
- 9: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1989.DAT:*
- 10: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1990.DAT:*
- 11: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1991.DAT:*
- 12: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1992.DAT:*
- 13: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1993.DAT:*
- 14: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1994.DAT:*
- 15: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1995.DAT:*
- 16: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1996.DAT:*
- 17: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1997.DAT:*
- 18: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1998.DAT:*
- 19: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA1999.DAT:*
- 20: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA2000.DAT:*
- 21: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA2001.DAT:*
- 22: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA2002.DAT:*
- 23: /SIDS2/gcdata/geneseq/geneseqP-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	711	100.0	134 18 AAV27371	Multi-epitope peptide
2	523.5	73.6	105 18 AAV27370	Multi-epitope peptide
3	320	45.0	80 18 AAV27369	Multi-epitope peptide
4	198.5	27.9	214 22 AAV69120	Cedar pollen aller
5	188	26.4	353 16 AAV75388	Japanese cedar pol
6	188	26.4	353 17 AAR81587	Cedar pollen aller
7	188	26.4	373 20 AAV25664	Cedar allergen 493
8	188	26.4	373 20 AAV25664	Japanese cedar aller
9	188	26.4	374 14 AAR31937	Cry j 1. Cryopome
10	188	26.4	374 15 AAR45541	i pollen all

ALIGNMENTS

RESULT 1	AAW27371	AAW27371 standard; peptide: 134 AA.
	XX	AAW27371;
	XX	DT 24-MAR-1998 (first entry)
	XX	DE Multi-epitope peptide used as immunotherapeutic agent #3.
	XX	KW Multi-epitope peptide; immunotherapeutic agent; allergic disease; T-cell epitope region; allergen; lymphocyte; immunoglobulin E.
	XX	CG Synthetic.
	XX	PN WO9732600(A1).
	XX	PD 12-SEP-1997.
	XX	PR 10-MAR-1997; 97WO-JP00740.
	PR 10-MAR-1996;	96JP-0080702.
	PA (MEIP)	MEIJI MILK PROD CO LTD.
	PI Dairiki, K., Iwama, A., Kino, K., Kume, A., Sone, T;	
	XX DR WPI; 1997-470495/43.	
	XX	Peptide immuno:therapeutic agent to treat allergic diseases -
	PT	PT contains multi-epitope peptide containing T cell epitope regions from different allergens

PS Claim 6; Page 32; 58pp; Japanese.

CC XX
CC The present sequence represents a multi-epitope peptide which is used as
CC a new immunotherapeutic agent. It comprises T cell epitope regions from 2
CC or more different allergens (preferably linked via arginine or lysine
CC dimers), where the T cell epitope regions have a positivity index
CC greater than 100 as measured in a patient group responding to the
CC allergen; have at least 70% reactivity with lymphocytes from patients
CC responding to the allergen; and are not reactive with immunoglobulin E
(IgE) antibodies from patients responsive to the allergen. The agent can
CC be used to prevent and treat a wide variety of allergic diseases, e.g. by
CC desensitisation. Side effects, e.g. those mediated by IgE, are reduced.

XX SQ sequence 134 AA;
Query Match 100.0%; Score 711; DB 18; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.7e-82; Mismatches 0; Indels 0; Gaps 0;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKVTVAQNQFGPNRRVFIKRVSNIHGRRIDIFASKNPHLQKNITGRRWNRIWQ 60
Db 1 MKVTVAFNQFGPNRRVFIKRVSNIHGRRIDIFASKNPHLQKNITGRRWNRIWQ 60

Qy 61 FAKLTGFTLMRRPLMIFSCAMNIKLMKMPMYIAGYKTFRGRRAEVSYVHNGAKFIRRV 120
Db 61 FAKLTGFTLMRRPLMIFSCAMNIKLMKMPYIAGYKTFRGRRAEVSYVHNGAKFIRRV 120

Qy 121 DGIIAVQNPASWK 134
Db 121 DGIIAVQNPASWK 134

Db 121 DGIIAVQNPASWK 134

RESULT 2
AAW27370
ID AAW27370 standard; peptide; 105 AA.
XX AC AAW27370;
XX DT 24-MAR-1998 (first entry)
XX DE Multi-epitope peptide used as immunotherapeutic agent #2.
XX KW Multi-epitope peptide; immunotherapeutic agent; allergic disease;
XX KW T-cell epitope region; allergen; lymphocyte; immunoglobulin E.
XX OS Synthetic.

OS Synthetic.
XX OS Synthetic.
XX PN WO9732600-A1.
XX PD 12-SEP-1997.
XX PF 10-MAR-1997; 97WO-JP00740.
XX PR 10-MAR-1996; 96JP-0080702.
XX PA (MEIP) MEIJI MILK PROD CO LTD.
XX PT Dairiki K, Iwama A, Kino K, Kume A, Sone T;
XX PI Dairiki K, Iwama A, Kino K, Kume A, Sone T;
XX DR WPI; 1997-470495/43.
XX PT Peptide immuno:therapeutic agent to treat allergic diseases -
XX PT contains multi-epitope peptide containing T cell epitope regions
XX from different allergens
XX Claim 6; Page 31; 58pp; Japanese.

XX PS The present sequence represents a multi-epitope peptide which is used as
XX a new immunotherapeutic agent. It comprises T cell epitope regions from 2
XX or more different allergens (preferably linked via arginine or lysine
XX dimers), where the T cell epitope regions have a positivity index
XX greater than 100 as measured in a patient group responding to the
XX allergen; have at least 70% reactivity with lymphocytes from patients
XX responding to the allergen; and are not reactive with immunoglobulin E
XX (IgE) antibodies from patients responsive to the allergen. The agent can
XX be used to prevent and treat a wide variety of allergic diseases, e.g. by
XX desensitisation. Side effects, e.g. those mediated by IgE, are reduced.

XX SQ Sequence 80 AA;

Query Match 45.0%; Score 320; DB 18; Length 80;

Best Local Similarity 53.7%; Pred. No. 6.1e-33; Mismatches 6; Indels 54; Gaps 2; Matches 72; Conservative

QY 1 MKVTQAFNQGPNEFPRVFKRVSNTIHRGRIDFASPKFHQLQNTIGTGRWRKGKRNWLO 60 RESULT 5
Db 1 MKVTQAFNQGPNEFPRVFKRVSNTIHRGRIDFASPKFHQLQNTIGTGRW 51 ID AAR75388
QY 61 FAKUJGFTLMGRPLWIIFSGNNMNTKLKMPWYIAGYKTFDGRRAEVSYVHUNGAKFIRR 120 ID AAR75388 standard; protein; 353 AA.
Db 52 -----1SLKL-----TSKIAARRV 66 AC AAR75388;
AC AC
QY 121 DGIIAYQNPASWK 134 XX
Db 67 DGIIAYQNPASWK 80 XX

RESULT 4
AAB6120 standard; protein; 214 AA.
XX
AC AAB69120;
XX
DT 23-APR-2001 (first entry)
DE Cedar pollen-allergen T cell epitope derived protein SEQ ID NO.61.
KW Japanese cedar; Cryptomeria japonica; cedar pollen allergen;
KW T cell epitope; anti-sugipollinosis.
XX
OS Cryptomeria japonica.
OS
XX
PR JP2000327699-A.
XX
FD 28-NOV-2000.
XX
PP 15-MAR-2000; 2000JP-0071710.
PR 15-MAR-1999; 99JP-0068316.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA (SANY) SANKYO CO LTD.
XX
DR WPI; 2001-185061/19.
DR N-FSDB; AAF59044.
XX
PT Novel peptide and its use -
XX
PS Example 11; Page 58-59; 75pp; Japanese.
XX
CC The present invention describes a peptide, its complex, derivative or its polymerize, where the peptide (I) has a formula of:
CC alpha1-alphab1-alpha2-alpha3-alpha4-alpha5-alpha6-alpha7
CC where alpha1 to alpha7 = amino acid sequence selected from amino acid sequences ranging from 11-19 amino acids derived from T cell epitopes derived from cedar (Japanese cedar - Cryptomeria japonica) pollen allergens. The peptide can be used in an anti-sugipollinosis agent. AAF59011 to AAF59062 and AAB69054 to AAB69121 represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 214 AA;

Query Match 27.9%; Score 198.5; DB 22; Length 214; Best Local Similarity 33.7%; Pred. No. 7.4e-17; Matches 55; Conservative 7; Mismatches 8; Indels 93; Gaps 5;

QY 1 MKVTQAFNQGPNEFPRVFKRVSNTIHRGRIDFASPKFHQLQNTIGTGRW 50 RESULT 6
Db 30 MKVTQAFNQGP-----DIFFASPKFHQLQNTIGTGRW 70 ID AAR81587
QY 51 -----RWNKRRIWL-----FAKUJGFTLMGRPLWIIFSGNNMNTKLKMPWYIAGYKTFDGRRAEVSYVHUNGAKFIRR 91 ID AAR81587 standard; Protein; 353 AA.

QY 92 VIAGYKTFDGRRAEVSYVHUNGAKFIRRVDGIAVQNPASWK 134 RESULT 5
Db 113 -----DBR-----GIIAYQNPASWK 128 ID AAR75388 standard; protein; 353 AA.
XX
AC AAR75388;
AC AC
XX
DT 12-MAR-1996 (first entry)
XX
DE Japanese cedar pollen allergen Cryj I.
XX
KW Japanese cedar; pollen allergen; Cryj I; T-cell epitope; peptides; prevention; treatment; cryptomeria pollinosis.
XX
OS Cryptomeria japonica.
XX
Key Location/Qualifiers
FH Peptide 61..75
FT Peptide /note= "T-cell epitope peptide"
FT Peptide 91..105 /note= "T-cell epitope peptide"
FT Peptide 106..120 /note= "T-cell epitope peptide"
FT Peptide 146..160 /note= "T-cell epitope peptide"
FT Peptide 211..225 /note= "T-cell epitope peptide"
FT Peptide 326..340 /note= "T-cell epitope peptide"
FT Peptide 335..346 /note= "T-cell epitope peptide"
FT Peptide 347..353 /note= "T-cell epitope peptide"
XX
PR JP07118295-A.
XX
PD 09-MAY-1995.
XX
PF 20-OCT-1993; 93JP-0262626.
PR 20-OCT-1993; 93JP-0262626.
XX
PA (MEIP) MEIJI MILK PROD CO LTD.
XX
DR WPI; 1995-203834/27.
XX
PT New cryptomeria pollen allergen T-cell epitope peptide - used for prevention, treatment and investigation of Japanese cedar pollinosis
XX Disclosure; Figs 1-2; 8pp; Japanese.
PS AAR5388 is the Japanese cedar pollen allergen Cryj I, from which the T-cell epitope peptides AAR8288-R89395 were derived. The peptides can be used for the prevention and treatment of cryptomeria pollinosis, and also for the investigation of pollinosis.
CC Sequence 353 AA;
SQ Query Match 26.4%; Score 188; DB 16; Length 353; Best Local Similarity 71.2%; Pred. No. 3.2e-15; Matches 37; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 73 RPLWIFSENMNTKLKMPWYIAGYKTFDGRRAEVSYVHUNGAKFIRRVDG 124 RESULT 6
Db 66 RPLWIFSENMNTKLKMPWYIAGYKTFDGRGAQVIGNGGPGVFKRVSNI 117 ID AAR81587 standard; Protein; 353 AA.

XX
AC AAR81587;
XX
DT 24-MAY-1996 (first entry)
XX
DE Cedar Pollen allergen B.
XX
KW antibody; pollinosis; therapy; immunotherapy.
OS Cryptomeria japonica.
XX
PN EP700929-A2.
XX
PD 13-MAR-1996.
XX
PF 08-SEP-1995; 95EP-0306295.
XX
PR 14-JUL-1995; 95JP-0200221.
PR 10-SEP-1994; 94JP-0242137.
PR 14-JUL-1995; 95JP-0200204.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PT Hino K, Saito S, Taniuchi Y;
XX
DR WPI; 1996-140976/15.
XX
PT New peptide(s) derived from cedar pollen allergens - activate
PT allergen-specific T-cells, but not allergen-specific IgE antibodies,
PT used for treating cedar pollinosis
XX
PS Claim 5; page 31-32; 36pp; English.
CC Synthetic peptides based on portions of cedar pollen allergens A
CC cedar allergen specific T-cells, but not allergen-specific IgE
CC antibodies. 6 Peptides (AAR81580-R81585) were identified as T-cell
CC epitopes. These peptides, plus subsequences (AAR81579) essential
CC for T-cell recognition, and homologous peptides (AAR81588-96) can
CC be used as immunotherapeutic agents to treat or prevent cedar
CC pollinosis, avoiding side-effects such as anaphylaxis.
XX
SQ Sequence 353 AA;

Query Match	26.4%	Score 188;	DB 17;	Length 353;
Best Local Similarity	71.2%	Pred. No.	3.2e-15;	
Matches	37;	Conservative	4;	Mismatches 11;
		Indels	0;	Gaps 0;

QY 73 RPLWIFSGMNNIKUKMPMYIAGYKTFDERRAENVSYVHNGAKRIRRVDGII 124
Db 66 RPLWIFSGMNNIKUKMPMYIAGYKTFDORGAGQVYIGNGGPCVFKRVSNVI 117

RESULT 7

AAV5564
ID AAV25664 standard; protein; 373 AA.

AC AAYZ5564;
XX
DT 30-SEP-1999 (first entry)

Cedar allergen 493634 Cry j 1B protein fragment.

Major histocompatibility complex; class II; desensitising; human; allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting; chironomidae; spider; mite; housefly; fruit fly; honeybee; screw worm fly; grain weevil; silkworm; bee moth; larva; mealworm; cat; cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig; mice; gerbil; vaccine; treatment; prevention; hypersensitivity; cedar.

OS Cedrus sp.

XX
PN WO934826-A1.
XX
PD 15-JUL-1999.
XX
PP 11-JAN-1999;
XX
PR 21-SEP-1998; 98GB-0020474.
PR 09-JAN-1998; 98GB-000045.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PT Kay AB, Larche M;
XX
DR WPI; 1999-458255/38.

XX
PT Desensitizing patients to polypeptide allergens
XX
PS Example 6; Page 73; 117pp; English.

This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for desensitising patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, food, stinging insects, the chironomidae (midge-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of Tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence represents a cedar (Cedrus sp.) allergen 493634 Cry j 1B.

XX
SQ Sequence 373 AA;

Query Match	26.4%	Score 188;	DB 20;	Length 373;
Best Local Similarity	71.2%	Pred. No.	3.5e-15;	
Matches	37;	Conservative	4;	Mismatches 11;
		Indels	0;	Gaps 0;

QY 73 RPLWIFSGMNNIKUKMPMYIAGYKTFDERRAENVSYVHNGAKRIRRVDGII 124
ID AAYZ5568
XX
Db 86 RPLWIFSGMNNIKUKMPMYIAGYKTFDORGAGQVYIGNGGPCVFKRVSNVI 137

RESULT 8

AAV25668
ID AAYZ5568 standard; protein; 373 AA.

AC AAYZ5568;
XX
DT 30-SEP-1999 (first entry)

Japanese cedar allergen 541803 Cry j 1 precursor protein fragment.

XX
KW Major histocompatibility complex; class II; desensitising; human; allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting; chironomidae; spider; mite; housefly; fruit fly; honeybee; screw worm fly; grain weevil; silkworm; bee moth; larva; mealworm; cat; cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig; mice; gerbil; vaccine; treatment; prevention; hypersensitivity; cedar.

OS Cedrus sp.

XX
PN WO934826-A1.
XX
PD 15-JUL-1999.
XX
PR 11-JAN-1999; 99WO-GB000080.
XX
PR 21-SEP-1998; 98GB-0020474.

XX

Novel peptide and its use -

Claim 1; page 39-40; 75pp; Japanese.

The present invention describes a peptide, its complex, derivative or its polymerize, where the peptide (I) has a formula of:
CC-alphai-alphai2-alphai3-alphai4-alphai5-alphai6-alphai7
where alphai to alphai7 = amino acid sequence selected from amino acid sequences ranging from 11-19 amino acids derived from T cell epitopes derived from cedar (Japanese cedar - Cryptomeria Japonica) pollen allergens. The peptide can be used in an antigusgipolliosis agent. AAF59011 to AAF5062 and AAB6904 to AAB9121 represent sequences used in the exemplification of the present invention.

Query Match 25.0%; Score 178; DB 22; Length 210;
 Best Local Similarity 32.5%; pred. No. 3e-14;
 Matches 53; Conservative 7; Mismatches 7; Indels 96; Gaps 6;

Search completed: May 5, 2003, 16:57:06

Job time : 47 secs

PRIOR FILING DATE: 1998-04-23
 PRIOR APPLICATION NUMBER: 60/083336
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083392
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083495
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083496
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083499
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083545
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083554
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083558
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083559
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083560
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083574
 PRIOR FILING DATE: 1998-04-30
 PRIOR APPLICATION NUMBER: 60/084366
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/084414
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084441
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084437
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084639
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084640
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084598
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085339
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 8.7%; Score 62; DB 9; Length 545;
 Best Local Similarity 25.7%; Pred. No. 47; Mismatches 49; Indels 24; Gaps 6;
 Matches 29; Conservative 11; Mismatches 49; Indels 24; Gaps 6;

Qy 87 LKMPMYIAGYKTFGRRAEVSYWHN--GAKFIRRVGII--AAYONPASWK 134
 Db 88 TKRPQVVTKGTLQKOMHVGKTPIQVFLGVPSRPPIGLRFAPPEPKW 140

RESULT 15
 US-10-174-590-58
 ; Sequence 58, Application US/10174590
 ; Publication No. US20030008352A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Palm, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3410R1C2
 CURRENT APPLICATION NUMBER: US/10/174,590
 CURRENT FILING DATE: 2002-06-18
 prior application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 58
 LENGTH: 545
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-174-590-58

Query Match 8.7%; Score 62; DB 9; Length 545;
 Best Local Similarity 25.7%; Pred. No. 47; Mismatches 49; Indels 24; Gaps 6;
 Matches 29; Conservative 11; Mismatches 49; Indels 24; Gaps 6;

Qy 45 TIGTGRRKNNRILQFAKL-----TGF-TLMGRPLWIFSGMN--IK 86
 Db 29 SFGTGT-SNPSPGVLINFNGLSTPATTSAPSSGGFGTGLFSKPAFTGFTLGGTNICAH 87

Qy 87 LKMPMYIAGYKTFGRRAEVSYWHN--GAKFIRRVGII--AAYONPASWK 134
 Db 88 TKRPQVVTKGTLQKOMHVGKTPIQVFLGVPSRPPIGLRFAPPEPKW 140

Search completed: May 5, 2003, 17:04:18
 Job time : 49 secs

QY 45 TICGRRMKNNRILWQFLKU-----TGF--TLMGRPMLWIFSGNNN---IK 86
 QY 29 SRTGTGS-SNPSTVGLNFGNLGSSTSPATTSAPSGCTGIGSKPATGFTLGGTGALH 87
 QY 87 LKXPMYLAGYKTFDGRRAEVSVHVN---GAKFIRUDGI--AAYONPASWK 134
 Db 88 TKEPQVVKYKGILQGKOMHVKGKTPIQVFLGVFFSRPLGLIRPAPPEPWK 140

RESULT 14
 US-09-978-189-254
 Sequence 254, Application US/09978189
 GENERAL INFORMATION:
 APPLICANT: Asikenaai, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gejber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Godowski, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Klujavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Sheldon, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 FILE REFERENCE: P2630P1C7
 CURRENT APPLICATION NUMBER: US/09/978,189
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/055311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077791
 PRIOR FILING DATE: 1998-03-12
 PRIOR APPLICATION NUMBER: 60/077804
 PRIOR FILING DATE: 1998-03-13
 PRIOR APPLICATION NUMBER: 60/078866
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078936
 PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078939
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079656
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079664
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079920
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079928
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079928
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079928
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080105
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080107
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080165
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080328
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080333
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080334
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/081070
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081094
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/0810971
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081195
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081203
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081229
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081955
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081817
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081819
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081952
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081838
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/082568
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082569
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082704
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082804
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082700
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082796

PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078936
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078939
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079656
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079664
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079663
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079728
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079786
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079920
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079923
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/080105
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080107
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080165
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080328
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080333
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080334
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080344
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080345
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080349
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080350
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083499
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083392
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083336
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/0833495
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/0833496
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083558
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083559
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083545
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083544
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083742
 PRIOR FILING DATE: 1998-04-30
 PRIOR APPLICATION NUMBER: 60/084366
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/084337
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/084414
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084441
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084637
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084639
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085339
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697
 Query Match 8.7%; Score 62; DB 9; Length 545;
 Best Local Similarity 25.7%; Pred. No. 47; Mismatches 49; Indels 24; Gaps 6;
 Matches 29; Conservative 11; Mismatches 49; Indels 24; Gaps 6;

Query Match 8.7%; Score 62; DB 9; Length 545;
 Best Local Similarity 25.7%; Pred. No. 47;
 Matches 29; Conservative 11; Mismatches 49; Indels 24; Gaps 6;
 Qy 45 TIGTGRRKNNRILQAKL-----TGT--TIGRPRWIISGMM--IK 86
 Db 29 SFGFGTS-SNPSVGLNFNLGNSSTPATTSAFSSGFTGTLGSKPATGFTGTTGNTGALH 87

Qy 87 LKOPMVIAGYKTFDGRRAEVYHVN--GAKFIRRDGT--AQNPAWK 134
 Db 88 TKRPQVVTKYSTLOGKOMVHGKPIQFLGPFSRPLGIRFAPEPPFWK 140

PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082700
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082796
 PRIOR FILING DATE: 1998-04-23
 PRIOR APPLICATION NUMBER: 60/083336
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083392
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083495
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083496
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083499
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083545
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083554
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083558
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083559
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083550
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083742
 PRIOR FILING DATE: 1998-04-30
 PRIOR APPLICATION NUMBER: 60/083666
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/084141
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084411
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084637
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084639
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084640
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084598
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085339
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

RESULT 13
 US-09-999-832A-254
 ; Sequence 254, Application US/09999832A
 ; Publication No. US20020192706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaoff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillah, Kenneth J.
 ; APPLICANT: Kijavan, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 ; CURRENT APPLICATION NUMBER: US 09/999, 832A
 ; CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066364
 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: 60/077450
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 60/077632
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077641
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077649
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077791
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/078004
 ; PRIOR FILING DATE: 1998-03-13
 ; PRIOR APPLICATION NUMBER: 60/078886

PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
; Sequence 254, Application US/09978697
; Patent No. US2002016928A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Behkennazi, Avi
APPLICANT: Bottstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillian, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Sheldon, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/064250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062449
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/07450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085570
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
; Query Match
; Best Local Similarity 8.7%; Score 62; DB 9; Length 545;
; Matchers 25; Conservative 11; Mismatches 49; Indels 24; Gaps 6
Qy 45 TIGTGRWRKNNRINWLOFAKL-----TGT-----TLMGRRLPLWIIFSGNMM--IK 86
Db 29 SFGTGTS-SNNSVGLNGNLGSTPATAPSSSGGTGFGLFSKPAITGFTGNTGALH 87
Qy 87 LKMPMVYTAGYKTFDGRRAEVSYVHN--GAKFIRRDGII-AAYQNPAWK 134
Db 88 TKRPQVWTKYGTILOGKOMHVKGTPIQVFLGVPPFSRPPLGILRFAPPEPKW 140

; LENGTH: 1375
; TYPE: PRT
; ORGANISM: streptococcus mutans
; US-09-740-274-4

Query Match. Best Local Similarity 24.8%; Pred. No. 1. 3e-02; Length 1375; Matches 34; Conservative 17; Mismatches 53; Indels 33; Gaps 8;

Qy 10 FGPNRRLV--IKRVEVNVLHGRRIDFASQNFRHQKNTG-----RRWNKRITL 59
Db 1185 FGQQWYFONGIMAVGSLTRVIG-AVQYFDASGFQAKGQFTTAQDGKLRYFDRDGGNQSN 1243
Qy 60 QFAKLTGFTLMGRPLMIFSGNMNKLKMPMYIAGKTFDGRAEVSYVHNG---AK 115
Db 1244 RFVR-----NSKGWLFPHN-----GVAVGTVIENGQRL---YFKPNVQAKGE 1286
Qy 116 FIRVUDGITAAYQNPAS 132
Db 1287 FIRDANGYL-RYDPPNS 1302

RESULT 10

US-09-978-295A-254

Sequence 254, Application US/09978295A

PATENT NO. US20020156606A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Garrison, Mary E.

APPLICANT: Godowski, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William T.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE REFERENCE: P2430PC1 CURRENT APPLICATION NUMBER: US/09/978-295A CURRENT FILING DATE: 2001-10-15 PRIOR APPLICATION NUMBER: 09/918855 PRIOR FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: 60/062250 PRIOR FILING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: 60/064249 PRIOR FILING DATE: 1997-11-03 PRIOR APPLICATION NUMBER: 60/065311 PRIOR FILING DATE: 1997-11-13 PRIOR APPLICATION NUMBER: 60/066364 PRIOR FILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: 60/077450 PRIOR FILING DATE: 1998-03-10 PRIOR APPLICATION NUMBER: 60/077632 PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080227
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568

US-10-121-032-15

; Sequence 15, Application US/10121032

; Patent No. US20020155550A1

; GENERAL INFORMATION:

; APPLICANT: Bylina, Edward J.

; APPLICANT: Swanson, Ronald W.

; APPLICANT: Mathur, Eric J.

; APPLICANT: Iam, David E.

; TITLE OF INVENTION: ENYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESS: Gray Cary Ware & Freidenrich LLP

; STREET: 4355 Executive Drive, Suite 1600

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/121,032

; FILING DATE: 09-Apr-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/134,078

; FILING DATE: 13-AUG-1998

; APPLICATION NUMBER: 08/949,026

; FILING DATE: 10-OCT-1997

; APPLICATION NUMBER: 60/056,916

; FILING DATE: 06-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Haile, Lisa A.

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 09010/024002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 858/677-1556

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 481 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULAR TYPE: protein

; FRAGMENT TYPE: Internal

; SEQUENCE DESCRIPTION: SEQ ID NO: 15:

; US-10-121-032-15

; Query Match

; Best Local Similarity 8.8%; Score 62.5; DB 9; Length 481;

; Matches 41; Conservative 28; Mismatches 59; Indels 63; Gaps 11;

; Oy 1 MKVTVAFNQGP---NRRVFIKRVS-NVIH----GRRIDIFASKN---PHLOK 43

; Db 77 IRVGVEWSRIFPKPTENKVVERDENGSTVHVVDVDDKAVERLBANKIAWHYVEMK 136

; Oy 44 NTIGTGR-----WNNR-----WL-----QFAKLGTGFTL-M 70

; Db 137 DWRVERGKLLNLXHPLPMLHNPIMVRMGPBRARSGMILNEFSVVERAKYAYIWM 196

; Oy 71 GRGP-LW-----IIFSGMNNTIKLKMPTIAGKTFDGRRAEVSYVIV--NGAKPFI 117

; Db 197 GELPVWSTMPNVPVYEQGYMFVKGGFPGYLSLEADKARRNMIQAHARAYDNIKRFS 256

; Oy 118 RRDGITAQO 128

; Do 257 KRPVGLIYAFQ 267

; US-10-993-037-15

; Query Match

; Best Local Similarity 8.8%; Score 62.5; DB 9; Length 481;

; Matches 41; Conservative 28; Mismatches 59; Indels 63; Gaps 11;

; Oy 1 MKVTVAFNQGP---NRRVFIKRVS-NVIH----GRRIDIFASKN---PHLOK 43

; Db 77 IRVGVEWSRIFPKPTENKVVERDENGSTVHVVDVDDKAVERLBANKIAWHYVEMK 136

; Oy 44 NTIGTGR-----WNNR-----WL-----QFAKLGTGFTL-M 70

; Db 137 DWRVERGKLLNLXHPLPMLHNPIMVRMGPBRARSGMILNEFSVVERAKYAYIWM 196

; Oy 71 GRGP-LW-----IIFSGMNNTIKLKMPTIAGKTFDGRRAEVSYVIV--NGAKPFI 117

; Db 197 GELPVWSTMPNVPVYEQGYMFVKGGFPGYLSLEADKARRNMIQAHARAYDNIKRFS 256

; Oy 118 RRDGITAQO 128

; Do 257 KRPVGLIYAFQ 267

; RESULT 9

; US-09-740-274-4

; Sequence 4, Application US/09740274

; Patent No. US20020031826A1

; GENERAL INFORMATION:

; APPLICANT: Nichols, Scott E.

; TITLE OF INVENTION: Glucan-containing Compositions and Paper

; FILE REFERENCE: 0357CPD

; CURRENT APPLICATION NUMBER: US/09/740,274

; CURRENT FILING DATE: 2000-12-19

; PRIORITY NUMBER: 09/210,361

; PRIORITY FILING DATE: 1998-12-11

; PRIORITY APPLICATION NUMBER: 09/007,999

; PRIORITY FILING DATE: 1998-01-15

; PRIORITY APPLICATION NUMBER: 08/478,704

; PRIORITY FILING DATE: 1995-06-07

; PRIORITY APPLICATION NUMBER: 09/009,620

; PRIORITY FILING DATE: 1998-01-20

; PRIORITY APPLICATION NUMBER: 08/485,243

; PRIORITY FILING DATE: 1995-06-07

; PRIORITY APPLICATION NUMBER: 09/008,172

; PRIORITY FILING DATE: 1998-01-16

; PRIORITY APPLICATION NUMBER: 08/482,711

; PUBLICATION NO. US2003078397A1

; GENERAL INFORMATION:

; RESULT 8

; US-10-093-037-15

; Sequence 15, Application US/10093037

; PUBLICATION NO. US2003078397A1

; GENERAL INFORMATION:

GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California Family of Taste Receptors
; TITLE OF INVENTION: TRR, a No. US20030022278A1
; FILE REFERENCE: 0231B-098010US
; CURRENT APPLICATION NUMBER: US/09/510,332
; CURRENT FILING DATE: 2000-02-22
; PRIORITY APPLICATION NUMBER: US 09/393,634
; PRIORITY FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO: 85
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat T2R05 (rGR05)
; US-09-510-332-85

RESULT 5
Query Match 8.9%; Score 63; DB 9; Length 309;
Best Local Similarity 28.4%; Pred. No. 18;
Matches 23; Conservative 15; Mismatches 33; Indels 10; Gaps 4;
Qy 52 WKNRNLQFAKUTGFTLGRPLWIFSGNNNIKU--KMPMIAKYKPFDGRRAE-V 106
Db 121 WKRNNNIVFVFLIGCHMS---WLFSFPVVKVNDKDNLYINSSWHMKSELI 175
Qy 107 SVVHVNAGAKFIRRVDGIIAY 127
Db 176 NYVFTNGGvPFLIMLIVCF 196

RESULT 6
US-10-114-893-73
; Sequence 73, Application US/10/114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Luisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Methberg, David
; APPLICANT: Tracy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vicki
; APPLICANT: Carlin-Buckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; EARLIER FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 73
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (135)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (179)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (318)
; US-10-114-893-73

RESULT 7
Query Match 8.8%; Score 62.5%; DB 9; Length 380;
Best Local Similarity 27.4%; Pred. No. 26;
Matches 20; Conservative 14; Mismatches 32; Indels 7; Gaps 3;
Qy 52 WKN--NRTWLQFAKUTGFTLGRPLWIFSGNNNIKU--GYKTFDGRRAEVS 107
Db 257 WKRNCNNIVFVFLIVFLTRVLVLPFL--HCTLVPLSLYPAFGYVFNSWMGLQ 313
Qy 108 YVHVNAGAKFIRR 120
Db 314 LLHIXWAYLILRM 326

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEX/FAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 811 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-10-011-366-7

Query Match 10.0%; Score 71; DB 9; Length 811;
 Best Local Similarity 21.7%; Pred. No. 6.6; Mismatches 64; Indels 44; Gaps 7;
 Matches 36; Conservative 22; Mismatches 64; Indels 44; Gaps 7;

Qy 3 VTVAFNQFGPNRVRVFKRSVNTTIGRRIIFASKNPHLOKNTCTGRAWKNNRNLWFLA 62
 Db 383 ITCERNNFYFDANNESKONTGVFKGPNFEGYFAPANTH-NNNIEQQAIVYQNKFTLNGK 441
 Qy 63 K-----LTGF-TLMGRSPPLWIFSGNN-----IKLKHMYIAG 95
 Db 442 KYFDNDSKAVTGWQTIDGKK----YYFNNTABAATGWQTIDGKKY'FNLNTAAATG 496
 Qy 96 YKTFDGRR-----AEVSYVHNGAKFIRRUGI--TAAYQNP 130
 Db 497 WQTIDGKKYYFNTNTFASTGTYTSINGKHFYFNTDGIMQIGVFKGP 542

RESULT 2
 US-10-011-366-6
 Sequence 6, Application US/10011366
 Publication No. US2003005493A1
 GENERAL INFORMATION:
 APPLICANT: Williams, James A.
 Kink, John A.
 TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPE
 OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE
 NUMBER OF SEQUENCES: 22
 DISEASE
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Medlen & Carroll
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/011366
 FILING DATE: 16-Nov-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/957,310
 FILING DATE: 23-Oct-1997
 APPLICATION NUMBER: US 08/329,154
 FILING DATE: 24-Oct-1994
 APPLICATION NUMBER: US 08/161,907
 FILING DATE: 02-Dec-1993
 APPLICATION NUMBER: US 07/985,321
 FILING DATE: 04-Dec-1992
 APPLICATION NUMBER: US 07/429,791
 FILING DATE: 31-Oct-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Ingolia, Diane E.
 REGISTRATION NUMBER: 40,027
 REFERENCE/DOCKET NUMBER: OPHD-01121
 TELECOMMUNICATION INFORMATION:

RESULT 3
 US-09-393-634-9
 Sequence 9, Application US/09393634
 Patent No. US20020051997A1
 GENERAL INFORMATION:
 APPLICANT: Zuker, Charles S.
 APPLICANT: Adler, Jon Elliot
 APPLICANT: Ryba, Nick
 APPLICANT: Mueller, Ken
 APPLICANT: Hoon, Mark
 APPLICANT: The Regents of the University of California
 APPLICANT: The Government of the United States of America
 APPLICANT: as represented by the Secretary of the
 APPLICANT: Department of Health and Human Services
 TITLE OF INVENTION: SF, a NO. US20020051997A1 et al Family of Taste Receptors
 FILE REFERENCE: 02307B-09800US
 CURRENT APPLICATION NUMBER: US/09/393,634
 CURRENT FILING DATE: 1999-09-10
 NUMBER OF SEQ ID NOS: 92
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 9
 LENGTH: 224
 TYPE: PRN
 ORGANISM: Rattus sp.
 FEATURE:
 OTHER INFORMATION: rat GROS

US-09-393-634-9

Query Match 9.0%; Score 64; DB 10; Length 224;
 Best Local Similarity 28.4%; Pred. No. 9.2; Mismatches 33; Indels 10; Gaps 4;
 Matches 23; Conservative 15; Mismatches 33; Indels 10; Gaps 4;

Qy 52 WKNRFLQFLKLSTGMRPLWIFSGNNMKL--KOMPMYIAGYKTFDERRAE--V 106
 Do 121 WLRKRINIVFPLIGCILMS---W-LFSPPVVVVKMVKDKMLYINSSWQIHMKSELT 175
 Qy 107 SYVHNGAKFIRRUGIAMI 127
 Do 176 NYVFTNGGVFLFIMVIGCF 196

RESULT 4
 US-09-510-332-85
 Sequence 85, Application US/09510332
 Publication No. US20030022278A1

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:59:07 ; Search time 46 Seconds

Sequence: 1 MKVIVAFNQFGPNRRVFIRR.....KFIRRDGIIAYQNPAWK 134

Scoring table: BLOSUM62

Gapext 0.0 , Gapext 0.5

Searched: 328255 seqs, 8628685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptcdatal2/pupbaa/US08_NEW_PUB_pep: *
2: /cgn2_6/ptcdatal2/pupbaa/PCT_NEW_PUB_pep: *
3: /cgn2_6/ptcdatal2/pupbaa/US06_NEW_PUB_pep: *
4: /cgn2_6/ptcdatal2/pupbaa/US07_PUBCOMB_pep: *
5: /cgn2_6/ptcdatal2/pupbaa/US07_NEW_PUB_pep: *
6: /cgn2_6/ptcdatal2/pupbaa/US07_PUBCOMB_pep: *
7: /cgn2_6/ptcdatal2/pupbaa/PCTU5_PUBCOMB_pep: *
8: /cgn2_6/ptcdatal2/pupbaa/US08_PUBCOMB_pep: *
9: /cgn2_6/ptcdatal2/pupbaa/US09_NEW_PUB_pep: *
10: /cgn2_6/ptcdatal2/pupbaa/US05_PUBCOMB_pep: *
11: /cgn2_6/ptcdatal2/pupbaa/US10_NEW_PUB_pep: *
12: /cgn2_6/ptcdatal2/pupbaa/US10_PUBCOMB_pep: *
13: /cgn2_6/ptcdatal2/pupbaa/US60_NEW_PUB_pep: *
14: /cgn2_6/ptcdatal2/pupbaa/US60_PUBCOMB_pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	71	10.0	811	9 US-10-011-366-7
2	71	10.0	2710	9 US-10-011-366-6
3	64	9.0	224	10 US-09-393-34-9
4	63	8.9	309	9 US-09-510-332-85
5	63	8.9	1121	8 US-08-915-048-A-2
6	62.5	8.9	380	9 US-10-114-893-73
7	62.5	8.8	481	9 US-10-121-032-15
8	62.5	8.8	481	9 US-10-093-037-15
9	62.5	8.8	1375	10 US-09-244-24-4
10	62	8.7	545	9 US-09-978-293A-254
11	62	8.7	545	9 US-09-978-293A-254
12	62	8.7	545	9 US-09-918-192A-254
13	62	8.7	545	9 US-09-939-832A-254
14	62	8.7	545	9 US-10-178-189-254
15	62	8.7	545	9 US-10-174-590-58
16	62	8.7	545	9 US-10-176-759-58
17	62	8.7	545	9 US-10-176-759-58
18	62	8.7	545	9 US-10-173-700-58
19	8.7	US-10-175-752-58		
20	62	8.7	545	9 US-10-176-422-58
21	62	8.7	545	9 US-10-176-427-58
22	62	8.7	545	9 US-10-176-913-58
23	62	8.7	545	9 US-10-180-532-58
24	62	8.7	545	9 US-10-174-588-58
25	62	8.7	545	9 US-10-175-739-58
26	62	8.7	545	9 US-10-175-743-58
27	62	8.7	545	9 US-10-176-438-58
28	62	8.7	545	9 US-10-176-432-58
29	62	8.7	545	9 US-10-176-747-58
30	62	8.7	545	9 US-10-176-750-58
31	62	8.7	545	9 US-10-176-935-58
32	62	8.7	545	9 US-10-176-987-58
33	62	8.7	545	9 US-10-176-991-58
34	62	8.7	545	9 US-10-176-932-58
35	62	8.7	545	9 US-10-176-933-58
36	62	8.7	545	9 US-10-184-635-58
37	62	8.7	545	9 US-10-173-635-58
38	62	8.7	545	9 US-10-173-697-58
39	62	8.7	545	9 US-10-173-697-58
40	62	8.7	545	9 US-10-176-932-58
41	62	8.7	545	9 US-10-176-933-58
42	62	8.7	545	9 US-10-176-934-58
43	62	8.7	545	9 US-10-176-935-58
44	62	8.7	545	9 US-10-176-936-58
45	62	8.7	545	9 US-10-176-937-58
46	62	8.7	545	9 US-10-176-938-58
47	62	8.7	545	9 US-10-176-939-58
48	62	8.7	545	9 US-10-176-940-58
49	62	8.7	545	9 US-10-176-941-58
50	62	8.7	545	9 US-10-176-942-58
51	62	8.7	545	9 US-10-176-943-58
52	62	8.7	545	9 US-10-176-944-58
53	62	8.7	545	9 US-10-176-945-58
54	62	8.7	545	9 US-10-176-946-58
55	62	8.7	545	9 US-10-176-947-58
56	62	8.7	545	9 US-10-176-948-58
57	62	8.7	545	9 US-10-176-949-58
58	62	8.7	545	9 US-10-176-950-58
59	62	8.7	545	9 US-10-176-951-58
60	62	8.7	545	9 US-10-176-952-58
61	62	8.7	545	9 US-10-176-953-58
62	8.7	545	9 US-10-176-954-58	

ALIGNMENTS

RESULT 1

US-10-011-366-7

; Sequence 7, Application US-10011366

; Publication No. US20030054493A1

; GENERAL INFORMATION:

; APPLICANT: Williams, James A.

; Kink, John A.

; TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPE

; OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE

; NUMBER OF SEQUENCES: 22

; DISEASE

; CORRESPONDENCE ADDRESS:

; ADDRESSE: Medlen & Carroll

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/Ms-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011_366

FILING DATE: 16-NO-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/957,310

FILING DATE: 23-OCT-1997

APPLICATION NUMBER: US 08/329,154

FILING DATE: 24-OCT-1994

APPLICATION NUMBER: US 08/61,907

FILING DATE: 02-DEC-1993

APPLICATION NUMBER: US 07/985,321

FILING DATE: 04-DEC-1992

APPLICATION NUMBER: US 07/429,791

FILING DATE: 31-OCT-1999

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: OPHD-01121

GenCore version 5.1.4_p5_4578
 copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 20, 2003, 12:56:55 ; Search time 12.6711 Seconds
 (without alignments)
 243.919 Million cell updates/sec

Title:	US-09-142-524D-152
Perfect score:	67
Sequence:	1 ISDISIKUTSGKIAS 15
Scoring table:	BLOSUM62
Gapop 10.0 , Gapext 0.5	
Searched:	671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters:	671580
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Minimum Match: 0%
Maximum Match: 100%	
Listing first 45 summaries	
Database :	SPREMBL 21;*
1:	sp_archeal:*
2:	sp_bacteria:*
3:	sp_fungi:*
4:	sp_human:*
5:	sp_invertebrate:*
6:	sp_mammal:*
7:	sp_mhc:*
8:	sp_organelle:*
9:	sp_phage:*
10:	sp_plant:*
11:	sp Rodent:*
12:	sp_virus:*
13:	sp_vertebrate:*
14:	sp_unclassified:*
15:	sp_rvirus:*
16:	sp_bacterioplasm:*
17:	sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	51	76.1	507	10 Q9FY19	Q9FY19 Juniperus a
2	45	67.2	251	16 Q8Z5W6	Q8Z5W6 salmonella
3	45	67.2	268	16 Q8ZN77	Q8ZN77 Salmonella
4	44	65.7	242	16 Q9Tn70	Q9Tn70 streptococc
5	43	64.2	275	16 Q9KE34	Q9KE34 rhizobium m
6	43	64.2	717	11 Q9CXJ4	Q9CXJ4 mus musculu
7	42	62.7	261	2 Q9R6G1	Q9R6G1 agrobacteri
8	42	62.7	1376	3 Q8XIP2	Q8XIP2 podospora a
9	40	59.7	134	16 Q8UDM0	Q8UDM0 agrobacteri
10	40	59.7	253	16 Q8ZEU3	Q8ZEU3 Yersinia pe
11	40	59.7	264	16 Q8RG16	Q8RG16 fusobacteri
12	40	59.7	278	9 Q8SCMB	Q8SCMB pseudomonas
13	40	59.7	299	16 Q9RRT2	Q9RRT2 staphylococ
14	40	59.7	299	16 Q931F9	Q931F9 staphylococ
15	40	59.7	317	3 Q9UD9	Q9UD9 schizosacch
16	40	59.7	1066	4 Q96DN5	Q96DN5 homo sapien

Query Match 76.1%; Score 51; DB 10; Length 507;
 Best Local Similarity 66.7%; Pred. 0.5%; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISDISIKUTSGKIAS 15

ALIGNMENTS

RESULT	ID	PRELIMINARY;	PRT;	AA.
1	Q9FY19	Q9FY19;	DT	01-MAR-2001 (TREMBLrel. 16, Created)
			DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
			DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
			DR	Pollen major allergen 2 protein precursor.
			GN	JN42.
			OS	Juniperus ashei (Ozark white cedar).
			OC	Bukaryota; Viridiplantae; Streptophyta; Tracheophyta;
			OC	Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Juniperus.
			OX	NCBI_TaxID=3101;
			RN	[1]
			RP	SEQUENCE FROM N.A.
			RC	TESSURE-MALE POLLEN;
			RX	MEDLINE=2043896; PubMed=10944464;
			RA	Yokoyama M., Mirahara M., Shimizu K., Kino K., Tsuno H.;
			RT	"Purification, Identification and cDNA cloning of Jun a 2, the second major allergen of mountain cedar pollen."
			RL	Biochem. Biophys. Res. Commun. 271:195-202(2000).
			CC	-!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES (POLYGLACTURONASES)
			DR	EMBL; AJ404653; CAC05582.1; -.
			DR	HSPB; P26509; 1BHE.
			DR	InterPro; IPR000743; GH28.
			DR	InterPro; IPR000948; Reg chr condens.
			DR	PEM; P00295; GLICO_HYDRO_26, 1.
			DR	PROSITE; PS05052; POLYGLACTURONASE; UNKNOWN_1.
			DR	PROSITE; PS0626; RCC1_2; UNKNOWN_1.
			KW	Cell wall; Glycosidae; -2; UNKNOWN_1.
			FT	Signal 1 54 POTENTIAL.
			SQ	SEQUENCE 507 AA; B220AA5A598FB5A CRC64;

RT	LIT2.;		
RL	Nature 413:852-856 (2001).		
DR	EMBL; AR008784; DAL2008.1; -.		
DR	InterPro; IPR003595; AAA_ATPase..		
DR	InterPro; IPR003439; ABC_transportr.		
DR	Pfam; PF00005; ABC_tran; 1.		
DR	Prodrom; PD000006; ABC_transporr; 1.		
KW	SMART; SM00382; AAA; 1.		
SQ	SEQUENCE 268 AA; 29750 MW; D5669D2448A74B28 CRC64;		
Query Match	Best Local Similarity 67.2%; Score 45; DB 16; Length 268; Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;		
Qy	1 LSDISLKUTSGKII 13		
Db	37 LSDVSLSPGKII 49		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CT18;		
RX	MEDLINE-21534947; PubMed=11677608;		
RA	Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihi M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaocha P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;		
RA	"Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar Typhi CT18.";		
RL	Nature 413:848-852 (2001).		
DR	EMBL; AL627072; CAD0543.1; -.		
DR	InterPro; IPR003593; AAA_ATPase..		
DR	InterPro; IPR003439; ABC_transportr.		
DR	Pfam; PF00005; ABC_tran; 1.		
DR	Prodrom; PD000006; ABC_transporr; 1.		
KW	SMART; SM00382; AAA; 1.		
ATP-binding; Complete proteome.	SEQUENCE 251 AA; 27731 MW; 4099397813CBBBO CRC64;		
Query Match	Best Local Similarity 67.2%; Score 45; DB 16; Length 251; Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;		
Qy	1 LSDISLKUTSGKII 13		
Db	20 LSDVSLSPGKII 32		
RESULT 3	.		
Q8ZNV7	PRELIMINARY;	PRT;	268 AA.
ID	Q8ZNV7;		
AC	DT 01-MAR-2002 (TREMBrel. 20, Created)		
DT	01-MAR-2002 (TREMBrel. 20, Last sequence update)		
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)		
DE	ABC superfamily (atp_bind) high affinity Zn transport protein.		
GN	ZINC OR STM1892.		
OS	<i>Salmonella typhimurium</i> .		
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.		
OC	Salmonella.		
OX	NEBI_TaxID602;		
RP	SEQUENCE N.A.		
RC	[1]		
RC	STRAIN=LT2 / SGSC1412 / ATCC 700720;		
RX	MEDLINE-21534948; PubMed=11677609;		
RA	McClelland M., Sanderson K.E., Spieth J.J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney B., Ryan E., Sun H., Florea L., Miller W., Stoenkong T., Nhan M., Waterston R., Wilson R.K.;		
RA	"Complete genome sequence of <i>Salmonella enterica</i> serovar Typhimurium		
RT	.		
RESULT 4	.		
Q9TN70	PRELIMINARY;	PRT;	242 AA.
ID	Q9TN70		
AC	DT 01-NOT-2001 (TREMBrel. 18, Created)		
DT	01-OCT-2001 (TREMBrel. 18, Last sequence update)		
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)		
DE	ABC transporter, ATP-binding protein.		
GN	SP2196.		
OS	<i>Streptococcus pneumoniae</i> .		
OC	Bacteria; Firmicutes; <i>Bacillus/Clostridium</i> group; Lactobacillales; Streptococcaceae; <i>Streptococcus</i> .		
OC	NCBI_TaxID313;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=TIG4;		
RX	MEDLINE-21357209; PubMed=11463916;		
RA	Tettelin H., Nelson K.B., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Hafft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapfel E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblum T.V., Anguilo S., Dickinson T., Hickey E.K., Holt T.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of <i>Streptococcus pneumoniae</i> ";		
RT	Science 293:498-506 (2001).		
RL	EMBL; AE007508; AAC76247.1; -.		
DR	TIGR; SP2196; -.		
DR	InterPro; IPR003593; AAA_ATPase..		
DR	InterPro; IPR003439; ABC_transportr.		
DR	InterPro; IPR001005; Myb_DNA_binding.		
DR	Pfam; PF00005; ABC_tran; 1.		
DR	SMART; SM00382; AAA; 1.		
DR	PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.		
DR	PROSITE; PS0037; MYB_1; UNKNOWN_1.		
KW	AIP-binding; Complete proteome.		
SQ	SEQUENCE 242 AA; 27519 MW; R88BD2FDD31DDB35 CRC64;		
Query Match	Best Local Similarity 65.7%; Score 44; DB 16; Length 242; Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;		
Qy	1 LSDISLKUTSGKIAS 15		
Db	19 LEDINQVLSGEVVS 33		
RESULT 5	.		
Q9KKE1	PRELIMINARY;	PRT;	275 AA.
ID	Q9KKE1;		
AC	.		

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE inner membrane ATPase protein (Histidine transport ATP-binding ABC transporter protein)
 GN H3V OR R02702 OR SMC00670.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Protoprobacteria; alpha subdivision; Rhizobiaceae group;
 NCBI_TAXID=382;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=RML000;
 RX MEDLINE=203309701; PubMed=10850986;
 RA Boncompagni E., Dupont L., Mignot T., Osteras M., Lambert A.,
 RA Poggi M.-C., Le Rudulier D.;
 RT "Characterization of a Sinorhizobium meliloti ATP-Binding Cassette Histidine Transporter Also Involved in Betaine and Proline Uptake.", J. Bacteriol. 182:3717-3725 (2000).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1031;
 RX MEDLINE=23196507; PubMed=11481430;
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelave V., Masuy D., Pohl T., Portetelle D., Puenier L., Purnelle B., Ramperger U., Renard C., Thebaud P., Vandebriel M., Weidner S., Galibert F.; RT "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 CC !- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL; AL1193; RAFF8099_1; -.
 DR EMBL; AL51791; CAC7281_1; -.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transportr.
 DR Pfam; PF00005; ABC_tran; 1.
 DR PRODOM; PD00006; ABC_transportr; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transport; Complete proteome.
 SQ SEQUENCE 275 AA; 30364 MW; 99441F5CCFP93790F CRC64;
 Query Match 64.2%; Score 43; DB 16; Length 275;
 Best Local Similarity 61.5%; Pred. No. 9.6;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LSDISIKLTSKGI 13
 Db 43 LNDVSLKIGAGKI 55
 RESULT 6
 O9CKX4 PRELIMINARY; PRT; 717 AA.
 AC O9CKX4;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone; 3222401P09, full insert sequence (RIKEN cDNA 4833412N02 gene).
 DE DE
 GN 4833412N02R1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TAXID=10090;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
 RX MEDLINE=2085660; PubMed=11217785;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Akakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S.,
 RA
 RA Mizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batyalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Borrelli D., Bojunga N., Carninci P., De Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garriboldi M., Gustinovich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzaelli J., Monbaerts P., Nordone P., Ring B., Rinewald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyoda A., Wang K.H., Weitz C., Whittaker C., Wilming L., Wyrshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S., Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BKIDNEY;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC015301; AAH15301_1; -.
 DR IHSPP; P13569; INED.
 DR MGD; MGIV:1521860; 4833412N02R1K.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001140; ABC_TransportrTM.
 DR InterPro; IPR003439; ABC_transportr.
 DR Pfam; PF00664; ABC_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR PRODOM; PD00006; ABC_transportr; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 DR ATTP-binding; 717 AA; 77995 MW; E573D4276B9558EB CRC64;
 SQ Query Match 64.2%; Score 43; DB 11; Length 717;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 LSDISIKLTSKIAS 15
 Db 472 LKDFTLKLPSGKIVA 486
 RESULT 7
 O9R6G1 PRELIMINARY; PRT; 261 AA.
 AC O9R6G1;
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DB TIOF58 protein.
 GN TIOF58.
 OC Agrobacterium tumefaciens.
 OC Plasmid pT-SAKURA.
 OC Bacteria; Protoprobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
 OC NCBI_TAXID=358;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=MAFF301001;
 RC STRAIN=MAFF301001;
 RX MEDLINE=10184752; PubMed=10721727;
 RA Suzuki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K., Katoch A., Yoshida K.;
 RT "Complete nucleotide sequence of a plant tumor-inducing Ti plasmid.";
 RN Gene 24:331-336(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF301001;
 RX MEDLINE=98193120; PubMed=95424202;

RA Suzuki K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
 RT "Novel structural difference between nosaline- and octopine-type trbU
 RT gene; construction of genetic and physical map and sequencing of
 RT trb/trbI and rep gene clusters of a new Ti plasmid pti-SAKURA";
 RL Biochim. Biophys. Acta 1396:1-7(1998).
 [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=MAFF301001;
 RA Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;
 RT "Genome structure of pti-SAKURA(I); Strategy for DNA sequencing of a
 RT Japanese cherry-Ti plasmid.";
 RL Nucleic Acids Symp. Ser. 37:155-160(1998).
 [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=MAFF301001;
 RA Ohta N., Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K.;
 RT "Genome structure of pti-SAKURA (III); Characteristics of T-DNA.;"
 RL Nucleic Acids Symp. Ser. 39:185-186(1998).
 [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=MAFF301001;
 RA Uraji M., Suzuki K., Ohta N., Hattori Y., Katoh A., Yoshida K.;
 RT "Genome structure of pti-SAKURA (IV); Characteristics of tra region.;"
 RL Nucleic Acids Symp. Ser. 39:187-188(1998).
 [6]
 RN SEQUENCE FROM N.A.
 RC STRAIN=MAFF301001;
 RA Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;
 RT "Genome structure of pti-SAKURA (V); Complete nucleotide sequence of
 RL plasmid pti-SAKURA's vir region in Agrobacterium tumefaciens.;"
 DR Nucleic Acids Symp. Ser. 39:265-266(1998).
 DR EMBL; AB016260; BA8723.1; -.
 DR InterPro; IPR003439; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transportr.
 DR Pfam; PF00005; ABC_tran_1.
 DR Prodrom; PDD00006; ABC_transporr_1.
 DR SMART; SM00382; AAA_1.
 DR ATP-binding; Plasmid.
 SQ SEQUENCE 261 AA; 27971 MW; 451054F02082BF9B CRC64;

Query Match 62.7%; Score 42; DB 2; Length 261;
 Best Local Similarity 61.5%; Pred. No. 14;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSDISLKUTSGK 13
 Db 35 LSDVSLKAWGKV 47

RESULT 9
 Q8UDMO Q8UDMO PRELIMINARY; PRT; 134 AA.
 AC Q8UDMO;
 DR 01-JUN-2002 (TRIMBLErel. 21, Last sequence update)
 DT 01-JUN-2002 (TRIMBLErel. 21, Last annotation update)
 DE Hypothetical protein Atu2104.
 GN ATU2104 OR AGR_C_3816.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 RN NCBItaxID=176299;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Biesen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendinnen J., Deatherage G., Gillett W., Grant C.,
 RA Kurtyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Neeter B.W.,
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58.;"
 RL Science 294:2317-2323 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gartung S., Miller N., Blanchard M., Mullin L.,
 RA Qurollo B., Goldmam B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 ID Q8X1P2 PRELIMINARY; PRT; 1376 AA.
 ID Q8X1P2;
 AC 01-MAR-2002 (TREMBREL_20, Created)
 DT 01-MAR-2002 (TREMBREL_20, Last sequence update)
 DT 01-MAR-2002 (TREMBREL_21, Last annotation update)
 DE Beta transducin-like protein HET-D2Y.
 GN HET-D.
 OS Podospora amserina.
 OC Sordariales; Lasiostaphyriaceae; Podospora.
 OC NEBI_TAXID=5145;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Espagne E., Baladre P., Begueret J., Turcq B.;
 RT "A new family of WD40 proteins implicated in vegetative
 incompatibility; evidence for a major role of WD40 repeat domain in
 RT the specificity of het-e and het-d genes.;"
 RT Submitted (Nov-2000) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AF323585; AAL37201.1; -.
 DR InterPro; IPR001680; WD40.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 12.
 DR PRINTS; PR00320; GPROTEINBRP.

RESULT 10
 Q8ZEU3

			PRELIMINARY;	PRT;	253 AA.
ID	Q8ZEU3				
AC	Q8ZEU3;				
DT	01-MAR-2002 (TREMBLrel. 20, Created)				
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)				
DE	High-affinity zinc uptake system ATP-binding protein.				
GN	ZNUC OR YP02060.				
OS	Versinia pestis.				
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;				
OC	Versinia.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CO-92 / BIOMR ORIENTALIS;				
RX	MEDLINE=21470413; PubMed=1158360;				
RA	Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,				
RA	Prentice M.B., Sebaihi M., James K.D., Church C., Mungall K.L.,				
RA	Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,				
RA	Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,				
RA	Feltwell T., Hanlin N., Holroyd S., Jagele K., Karlyshev A.V.,				
RA	Leather S., Moule S., Oyston P.C.F., Quail M., Ruttyford K.,				
RA	Simmonds M., Shelton J., Stevens K., Whitehead S., Barrell B.G.;				
RT	"Genome sequence of <i>Versinia pestis</i> , the causative agent of plague.";				
RL	Nature 413:523-527(2001).				
DR	EMBL; AJ44151; CAC0872.1; --.				
DR	IPR03593; AAA; ATPase.				
DR	InterPro; IPR03439; ABC_transportr.				
DR	PFAM; PF00005; ABC_tran; 1.				
DR	PRODOM; PRO0006; ABC_transportr; 1.				
DR	SMART; SM00382; AAA; 1.				
SQ	ATP-binding; Complete proteome.				
SQ	SEQUENCE 253 AA; 27620 MW; 15B2023B927169B CRC64;				
Query Match	59.7%; Score 40; DB 16; Length 253;				
Best Local Similarity	69.2%; Pred. No. 32;				
Matches	9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;				
Qy	1 LSDISLKLTSGK 13				
Db	21 LNDISLSLRPGK 33				
RESULT 11					
Q8RG16					
ID	Q8RG16	PRELIMINARY;	PRT;	264 AA.	
AC	Q8RG16;				
DT	01-JUN-2002 (TREMBLrel. 21, Created)				
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Iron(III) dicitrato transport ATP-binding protein fecE.				
GN	FN0307.				
OS	Fusobacterium nucleatum (subsp. nucleatum).				
OC	Bacteria; Fusobacteria; Fusobacterium.				
OX	NCBI_TaxID=76856;				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 25586;				
RX	MEDLINE=21886394; PubMed=11899109;				
RA	Kapatral V., Ivanova N., Reznik G., Los T., Lykidis A.,				
RA	Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,				
RA	Larsen N., D'Souza M., Walunas T., Pusch G., Haeckorn R.,				
RA	Fonstein M., Kyriakis N., Overbeek R.,				
RT	"Genome sequence and analysis of the oral bacterium <i>Fusobacterium nucleatum</i> strain ATCC 25586."				
RT	J. Bacteriol. 184:2005-2018(2002).				
DR	EMBL; AB010543; AAB04513.1; -.				
KW	ATP-binding; Complete proteome.				
SQ	SEQUENCE 264 AA; 30095 MW; 04C8BDA94F121B53 CRC64;				
Query Match	59.7%; Score 40; DB 16; Length 264;				
Best Local Similarity	61.5%; Pred. No. 33;				
Matches	8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;				
QY	1 LSDISLKLTSGK 13				
DB	22 LNDISLSLRPGK 34				
RESULT 12					
Q8SCMB					
ID	Q8SCMB	PRELIMINARY;	PRT;	278 AA.	
AC	Q8SCMB;				
DT	01-JUN-2002 (TREMBLrel. 21, Created)				
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Phage phiKZ.				
DR	Pseudomonas phage phiKZ.				
OS	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.				
RR	NCBI_TaxID=169683;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RK	MEDLINE=2191455; PubMed=11916376;				
RA	Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,				
RA	Bourkaltseva M.V., Sykilinda N.N., Krylov V.V., Volkert G.;				
RA	"The genome of bacteriophage phiKZ of <i>Pseudomonas aeruginosa</i> ,"; J. Mol. Biol. 341:1-19(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,				
RA	Bourkaltseva M.V., Sykilinda N.N., Krylov V.V., Volkert G.;				
RA	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; AR399011; AAL8185.1; -.				
SQ	SEQUENCE 278 AA; 31883 MW; C7A2CA9FDE57AD5A CRC64;				
Query Match	59.7%; Score 40; DB 9; Length 278;				
Best Local Similarity	53.8%; Pred. No. 35;				
Matches	7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;				
QY	3 DISLKLUKNGKIAS 15				
DB	220 DVLIKUTNGKVYS 232				
RESULT 13					
Q99RT2					
ID	Q99RT2	PRELIMINARY;	PRT;	299 AA.	
AC	Q99RT2;				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Hypothetical protein SA2132.				
GN	SA2132.				
OS	Staphylococcus aureus (strain N315).				
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;				
OC	Staphylococcus.				
OK	NCBI_TaxID=158879;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21311952; PubMed=11418146;				
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,				
RA	Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,				
RA	Matsuura H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Uji Y.,				
RA	Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,				
RA	Hirakawa H., Kuwahara S., Goto S., Yabuzaki J., Kanemitsu M.,				
RA	Yamasita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,				
RA	Ogasawara N., Hayashi H., Hiramatsu K.;				
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus aureus."				
RT	Lancet 357:1228-1240(2001).				
DR	EMBL; AP00136; BAB03433.1; -.				
DR	InterPro; IPR03593; AAA; ATPase.				
DR	PFAM; PF00005; ABC_tran; 1.				
DR	PRODOM; PRO0006; ABC_transportr; 1.				
DR	SMART; SM00382; AAA; 1.				

DR PROSITE; PS00211; ABC TRANSPORTER; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 299 AA; 33723 MW; BA8EFC5B01FFD7C CRC64;

Query Match	59.7%	Score 40;	DB 16;	Length 299;
Best Local Similarity	61.5%;	Pred. No. 37;	DB 3;	Length 317;
Matches	8;	Conservative	2;	Mismatches

Qy 1 LSDISLKLTSKTI 13
 ::|||||:|||:
 Db 18 VNDISLKLTSKTI 30

RESULT 14

0931F9 PRELIMINARY; PRT; 299 AA.

ID Q931F9; PRELIMINARY; PRT; 299 AA.

AC Q931F9; PRELIMINARY; PRT; 299 AA.

DT 01-DEC-2001 (TREMBrel. 19, Created)
 01-DEC-2001 (TREMBrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)

DE Hypothetical protein SAV2341.

GN SAV2341.

OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 Staphylococcaceae; Staphylococcus.

OC NCBI_TaxID=158878;

OX NCBI_TaxID=158878;

RN [1]

SEQUENCE FROM N.A. PubMed=11418146;

RX MEDLINE=21311952;

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 Sekimizu K., Hirakawa H., Kuwara S., Goto S., Rabuzaki J.,
 Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 Hattori M., Ogawara N., Hayashi H., Hiramatsu K.;
 "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus ", Lancet 357:1225-1240(2001).

RL EMBL; AP003365; BAB8503; 1; -.

DR Interpro; IPR003439; ABC transport.

DR ProDom; PD000006; ABC transporter; 1.

DR PROSITE; PS00211; ABC TRANSPORTER; UNKNOWN_1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 299 AA; 33757 MW; 798EFC5B01FFD7A CRC64;

Query Match 59.7%; Score 40; DB 16; Length 299;
 Best Local Similarity 61.5%; Pred. No. 37;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LSDISLKLTSKTI 13
 ::|||||:|||:
 Db 18 VNDISLKLTSKTI 30

RESULT 15

Q9UD9 PRELIMINARY; PRT; 317 AA.

ID Q9UD9; PRELIMINARY; PRT; 317 AA.

AC Q9UD9; PRELIMINARY; PRT; 317 AA.

DT 01-MAY-2000 (TREMBrel. 13, Created)
 01-MAY-2000 (TREMBrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBrel. 13, Last annotation update)

DE Hypothetical 37.0 kDa protein.

GN SPBC17G8.13C.

OS Schizosaccharomyces pombe (Fission Yeast).
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomycetes; NCBI_TaxID=4896;
 [1]

OC Schizosaccharomyces pombe (Fission Yeast).
 Schizosaccharomyces pombe (Fission Yeast);
 Schizosaccharomycetes; Schizosaccharomycetaceae;
 Schizosaccharomycetes; NCBI_TaxID=4896;
 [1]

RN SQUENCE FROM N.A.

RP STRAIN=972H-;

RA Wood V., Rajandream M.A., Barrell B.G., Volckaert G.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL109846; CAB5811.1; -.

KW Hypothetical protein.

SQ SEQUENCE 317 AA; 37009 MW; C4356E2E97057126 CRC64;

Query Match	59.7%	Score 40;	DB 3;	Length 317;
Best Local Similarity	61.5%;	Pred. No. 40;	DB 3;	Length 317;
Matches	8;	Conservative	2;	Mismatches
Indels	0;	Gaps	0;	

Qy 1 LSDISLKLTSKTI 13
 ::|||||:|||:
 Db 297 LSDIQLRLANV3KV 309

Search completed: April 20, 2003, 13:13:23
 Job time : 14.6711 secs